

Post-processing: Minimum Match 0% Maximum Match 100%						
Listing first 45 summaries						
Database :	A_Geneseq_29Jan04: 1: geneseqD1980s;* 2: geneseqDP1990s;* 3: geneseqD2000s;* 4: geneseqD2001s;* 5: geneseqDP2002s;* 6: geneseqD2003as;* 7: geneseqD2003bs;* 8: geneseqDP2004s;*	Minimum Match 0% Maximum Match 100%				
Scoring table:	BLOSUM62 Gapext 10.0 , Gapext 0.5					
Searched:	1586107 seqs, 282547505 residues					
Total number of hits satisfying chosen parameters:	1586107					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Pred. No.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
Result No.	Score	Query Length	DB ID	Description		
1	164	100.0	31	Aaw39910 Peptide r		
2	164	100.0	100	Aaw88231 HIV-1 co-		
3	164	100.0	184	Aaw27406 Inactive		
4	164	100.0	215	Aaw27408 Inactive		
5	164	100.0	215	Aaw88238 HIV-1 co-		
6	164	100.0	268	Adc1044 Human NOV		
7	164	100.0	268	Adc10144 Human NOV		
8	164	100.0	352	Aaw27407 Human CCR		
9	164	100.0	352	Aaw27123 Human che		
10	164	100.0	352	Aaw23835 Human CCR		
11	164	100.0	352	Aaw88232 HIV-1 co-		
12	164	100.0	352	Aae07048 Human G-P		
13	164	100.0	352	Aag80111 Human CCR		
14	164	100.0	352	Aae04321 Human che		
15	164	100.0	352	Aae07039 Human G-P		
16	164	100.0	352	Aab46858 Human HDG		
17	164	100.0	352	Aab56342 Human G-P		
18	164	100.0	352	Aab83354 Human CCR		
19	164	100.0	352	Aab82949 Human HIV		
20	164	100.0	352	Aau97152 Human G-P		
21	164	100.0	352	Aam5229 Human CCR		
22	164	100.0	352	Aam5228 Human CCR		
23	164	100.0	352	Abg70597 Human G-P		
24	164	100.0	352	Abg92883 Human imm		
25	164	100.0	352	Aae25811 Human G-P		

ALIGNMENTS

RESULT 1
ID Aaw39910 standard; peptide; 31 AA.
XX
AC AAW39910;
XX
DT 06-JUL-1998 (first entry)
XX
DE Peptide representing an extracellular domain of C-C CKR-5.
XX
KW Chemokine receptor; C-C CKR-5; Human Immunodeficiency Virus; HIV-1;
KW CD4+ cell; inhibition; HIV-1 infection; beta-chemokine;
KW non-synctium-inducing HIV-1 strain; treatment.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN WO9747319-A1.
XX
PD 18-DEC-1997.
XX
PP 13-JUN-1997; 97WO-US010619.
XX
PR 14-JUN-1996; 96US-0019941P.
XX
PR 14-JUN-1996; 96US-0066590.
XX
PA (PROG-) PROGENICS PHARM INC.
(AARO-) AARON DIAMOND AIDS RES CENT.
XX
PI Allaway GP, Dragic T, Litwin VM, Maddon PJ, Moore JP, Trkola A;
XX
DR WPI; 1998-086551/08.
XX
PT Synthetic Peptides AAW39910-13 represent the 4 extracellular domains of human chemokine receptor CCR5. C-C CKR-5 is capable of inhibiting the fusion of Human Immunodeficiency Virus (HIV)-1 to CD4+ cells and thus inhibiting HTLV-1 infection of the cells. It is suggested that C-C CKR-5 functions as a beta-chemokine-sensitive secondary receptor for primary non-synctium-inducing HIV-1 strains. The synthetic peptides were tested for their ability to inhibit membrane fusion mediated by the envelope glycoproteins of the LAI or JR-FL strains of HIV-1 using a resonance energy transfer assay. Specific inhibition of fusion mediated by the JR-FL envelope glycoprotein was seen using the EC2 peptide but not other

RESULT 2						
Query AAW88231						
Query Match	100.0%	Score 164;	DB 2;	Length 31;		
Best Local Similarity	100.0%	Pred. No. 9e-18;				
Matches	31;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
Ov	1 MDYQVSSPIYDINYTTSEPCQKXINVQIAAR 31					
Db	1 MDYQVSSPIYDINYTTSEPCQKXINVQIAAR 31					
Sequence 31 AA:						
XX	AAW88231	standard;	protein;	100 AA.		
XX	AAW88231;					
AC						
XX						
DT	15-MAR-1999	(first entry)				
XX	HIV-1 co-receptor CCR5 variant CCR5m03.					
DE						
KW	HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;					
KW	gene therapy; human.					
XX						
OS	Homo sapiens.					
XX						
PH	Key	Location/Qualifiers				
FT	Domain	32..56				
FT		/note= "transmembrane domain 1"				
FT	Domain	67..87				
FT		/note= "transmembrane domain 2"				
PN	W09854317-A1.					
XX						
PR	03-DEC-1998.					
XX						
PA	29-MAY-1998;	98WO-EP003437.				
XX						
PR	30-MAY-1997;	97US-0048057P.				
XX						
PA	(MOND-) FOND MONDIALE RECH & PREVENTION SIDA.					
XX						
PT	Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;					
XX						
DR	WPI:1999-059835/05.					
DR	N-PSDB; AAW88231.					
XX						
PT	New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection.					
XX						
PS	Claim 2; Page 37; 55pp; English.					
XX						
CC	This is the amino acid sequence of a CCR5 variant protein, designated CCR5m303, that comprises the first two transmembrane domains of wild-type CCR5 (see AAW88232), but lacks transmembrane domains 3-7. CCR5 serves as a co-receptor for infection by macrophage-tropic (M-tropic) strains of CC HIV-1; the presence of the CCR5m303 variant allele (see AAV84125) with CC the wild type CCR5 allele in an individual shows positive correlation CC with resistance to infection with M-tropic HIV-1 strains, and may CC indicate slower progression of the disease. The detection of CCR5 CC variants may be used to identify individuals at lower risk of infection CC relative to the general population who, if infected, may exhibit slower CC progression to AIDS. Probes and primers (see AAV84127-36) are provided CC for use in diagnostic methods for detecting the presence of such CC variants. A method is provided for inhibiting HIV-1 infection of a cell CC expressing the CCR5 receptor. This involves introducing a nucleic acid CC encoding a CCR5 variant into the cell, thereby reducing the number of CC functional CCR5 molecules present on the cell surface.					

XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
 KW antihypertensive; gene therapy; antisense therapy; thymomimetic; NOVX;
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 KW inflammatory disorder; chromosome mapping; tissue typing;
 KW predictive medicine.

OS Homo sapiens.

PN WO2003000842-A2.
 XX

PD 03-JAN-2003.

PP 04-JUN-2002; 2002WO-US017443.
 XX

PR 04-JUN-2001; 2001US-0295607P.

PR 04-JUN-2001; 2001US-029561P.

PR 06-JUN-2001; 2001US-029640P.

PR 06-JUN-2001; 2001US-0296418P.

PR 07-JUN-2001; 2001US-0296575P.

PR 11-JUN-2001; 2001US-0297414P.

PR 12-JUN-2001; 2001US-0295513P.

PR 12-JUN-2001; 2001US-0297567P.

PR 14-JUN-2001; 2001US-0298285P.

PR 15-JUN-2001; 2001US-0298538P.

PR 18-JUN-2001; 2001US-0299333P.

PR 19-JUN-2001; 2001US-0299230P.

PR 21-JUN-2001; 2001US-0299919P.

PR 22-JUN-2001; 2001US-0300177P.

PR 26-JUN-2001; 2001US-0300983P.

PR 28-JUN-2001; 2001US-0301540P.

PR 03-JUL-2001; 2001US-0301550P.

PR 03-JUL-2001; 2001US-0302951P.

PR 31-JUL-2001; 2001US-0308830P.

PR 14-SEP-2001; 2001US-0322291P.

PR 25-SEP-2001; 2001US-0324669P.

PR 03-DEC-2001; 2001US-0371347P.

PR 14-DEC-2001; 2001US-0341563P.

PR 21-FEB-2002; 2002US-0358656P.

PR 21-FEB-2002; 2002US-0359122P.

PR 22-FEB-2002; 2002US-0358978P.

PR 22-FEB-2002; 2002US-0359014P.

PR 22-FEB-2002; 2002US-0359055P.

PR 22-FEB-2002; 2002US-0359123P.

PR 27-FEB-2002; 2002US-0359944P.

PR 01-MAR-2002; 2002US-0310838P.

PR 12-MAR-2002; 2002US-0363430P.

PR 12-MAR-2002; 2002US-0363676P.

PR 10-APR-2002; 2002US-0371346P.

PR 04-JUN-2002; 2002US-0379444P.

XX (CURAGEN CORP.

PI Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;

PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangollie EA;

PI Gerlach VL, Goran L, Guo X, Herrmann JL, Hajt T, Ji W, Kekuda R;

PI Khrantsov NV, Li L, Liu X, Malyanik UM, Miller CE, Millet I;

PI Ort T, Padigaru M, Paturajan M, Pena CBA, Rastelli I, Rieger DK;

PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;

PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;

PI Burgess CB, Lepley DM;

XX DR WPI; 2003-210149/20.

XX N-PSDB; ADC10141.

XX New isolated NOVX polypeptides and nucleic acid molecules useful for
 PT treating, preventing and diagnosing pathological conditions with NOVX-
 PT associated disorders, such as cancer, obesity, diabetes and inflammatory
 PT or CNS diseases.

XX Claim 1; SEQ ID NO 162; 772pp; English.
 XX

CC The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOVX
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 CC endocrine, CNS and inflammatory disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to one of the
 CC polypeptides of the invention.

XX

SQ Sequence 268 AA;

Query Match 100.0%; Score 164; DB 7; Length 268;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQSSPIYDINYTSEPCOKINYTQIAAR 31
 Db 1 MDYQSSPIYDINYTSEPCOKINYTQIAAR 31

RESULT 7

ADC10144

ID ADC10144 standard; protein; 268 AA.

XX

AC ADC10144;

XX

DT 18-DEC-2003 (first entry)

XX

Human NOVX polypeptide SEQ ID NO: 164.

DE

KW cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;

KW antiinflammatory; gene therapy; antisense therapy; thymomimetic; NOVX;

KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;

KW inflammatory disorder; chromosome mapping; tissue typing;

KW predictive medicine.

XX

Homo sapiens.

OS

XX

XX

PN WO2003000842-A2.

XX

PD

03-JAN-2003.

XX

PF

04-JUN-2002;

2002WO-US017443.

XX

PR 22-FEB-2002; 2002US-0359035P.
 PR 22-FEB-2002; 2002US-0359121P.
 PR 27-FEB-2002; 2002US-0359964P.
 PR 01-MAR-2002; 2002US-0360858P.
 PR 12-MAR-2002; 2002US-0361340P.
 PR 12-MAR-2002; 2002US-0363430P.
 PR 10-MAY-2002; 2002US-0371346P.
 PR 04-JUN-2002; 2002US-0379444P.
 PR 04-JUN-2002; 2002US-0379444P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
 PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
 PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;
 PI Khramtsov NV, Li L, Liu X, Malyanbar UM, Miller CB, Millet I;
 PI Ort T, Padigaru M, Patterson M, Peña CEA, Rastelli L, Rieger DK;
 PI Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
 PI SPYTE KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
 PI Burgess CE, Lepley DM;
 XX
 DR WPI; 2003-21-0149/20.
 DR N-PSDB; ADC10143.
 XX
 PT New isolated NOVX polypeptides and nucleic acid molecules useful for
 PT treating, preventing and diagnosing pathological conditions with NOVX-
 PT associated disorders, such as cancer, obesity, diabetes and inflammatory
 PT or CNS diseases.
 XX
 PS Claim 1; SEQ ID NO 164; 772pp; English.
 XX
 CC The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOVX
 CC peptide is useful for treating or preventing a pathology associated with
 CC the polypeptide e.g. disorders associated with aberrant expression
 CC or endocrine, CNS and inflammatory disorders. They can also be used in
 CC - various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to one of the
 CC polypeptides of the invention.
 XX
 SQ Sequence 268 AA;

Query Match Score 164; DB 7; Length 268;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYQVSSPIVDINYXTSEPCOKINVQIAAR 31
 1 MDYQVSSPIVDINYXTSEPCOKINVQIAAR 31

Db 1 MDYQVSSPIVDINYXTSEPCOKINVQIAAR 31

RESULT 9
 AAW27123 standard; protein; 352 AA.
 ID AAW27123
 XX
 AC AAW27123;
 XX
 DT 14-DEC-1997 (first entry)
 DE Human Chemokine receptor 88C.
 XX
 OS Homo sapiens.
 FH Key
 FT Domain
 FT /label= Extracellular_domain
 PT Domain
 PT 56 .67
 PT /label= Intracellular_domain
 PT Domain
 PT 89 .112
 PT /label= Extracellular_domain
 PT Domain
 PT 125 .145
 PT /label= Intracellular_domain
 PT Domain
 PT 166 .191
 PT /label= Extracellular_domain
 PT Domain
 PT 213 .235
 PT /label= Intracellular_domain
 PT Domain
 PT 259 .280

RESULT 8
 AAW27407
 ID AAW27407 standard; protein; 352 AA.
 XX
 AC AAW27407;
 DT 14-APR-1998 (first entry)
 XX
 DE Human CCR5.
 XX
 KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
 KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO9732019-A2.
 XX

XX HIV-1 co-receptor CCR5.
 XX HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 KW gene therapy; human.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Domain 32..56
 FT Domain /note= "transmembrane domain 1"
 FT Domain 67..87
 FT /note= "transmembrane domain 2"
 FT Misc-difference
 FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA (Stop) in CCR5m303"
 FT Domain 103..124
 FT /note= "transmembrane domain 3"
 FT Domain 142..167
 FT /note= "transmembrane domain 4"
 FT Domain 200..223
 FT /note= "transmembrane domain 5"
 FT Domain 236..260
 FT /note= "transmembrane domain 6"
 FT Domain 275..301
 FT /note= "transmembrane domain 7"
 XX WO9854317-A1.
 XX PD 03-DEC-1998.
 XX PP 29-MAY-1998;
 XX PR 30-MAY-1997;
 XX PA (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 PI Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
 DR WPI; 1999-059835/05.
 DR N-PSDB; AA784126.
 XX PT New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection.
 PS Disclosure: Page 34-35; 55pp; English.

This is the amino acid sequence of wild-type human CCR5, which serves as a co-receptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. The invention relates to the identification of a CCR5 variant (see AAW8231), designated CCR5m303, comprising the first two transmembrane domains of wild-type CCR5, but lacking transmembrane domains 3-7. The presence of the CCR5m303 variant with the wild type CCR5 allele shows a positive correlation with resistance to infection with M-tropic HIV-1 strains, and may indicate slower progression of the disease. The detection of CCR5 variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS. Probes and primers (see AAV84127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCR5 receptor. This involves introducing a nucleic acid encoding a CCR5 variant into the cell, thereby reducing the number of functional CCR5 molecules present on the cell surface

XX Sequence 352 AA;

CC Query Match 100..0%; Score 164; DB 2; Length 352;
 CC Best Local Similarity 100..0%; Pred. No. 1..7e-16;
 CC Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPPIVDINYTTSEPCOKINVKQIAAR 31
 Db 1 MDYQVSSPPIVDINYTTSEPCOKINVKQIAAR 31

XX Sequence 352 AA;

XX RESULT 12
 ID AAE07048 standard; protein; 352 AA.
 XX AC AAE07048;
 XX DT 16-OCT-2001 (first entry)
 XX DE Human G-protein chemokine receptor (CCRS) HDGNR10 protein #2.
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vasoconstrictor; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; haematointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.

XX KW Homo sapiens.

XX PN WO200158916-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004153.

XX PR 09-FEB-2000; 2000US-0181258P.

XX PR 09-MAR-2000; 2000US-0187999P.

XX PR 22-SEP-2000; 2000US-0234336P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Roschke V, Li Y, Ruben SM;

XX DR WPI; 2001-48896/67-A.
 DR N-PSDB; AA713299.

XX PT Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

XX PS Example 40; Page 504-505; 518pp; English.

XX CC The invention relates to human G-protein chemokine receptor (CCRS) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, muscular sclerosis (myocardial ischaemia) and ulcerative colitis). The present sequence is human CCR5 HDGNR10 protein

XX Sequence 352 AA;

CC Query Match 100..0%; Score 164; DB 2; Length 352;
 CC Best Local Similarity 100..0%; Pred. No. 1..7e-16;
 CC Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPPIVDINYTTSEPCOKINVKQIAAR 31
 Db 1 MDYQVSSPPIVDINYTTSEPCOKINVKQIAAR 31

XX Sequence 352 AA;

Query Match	100.0%	Score 164; DB 4; Length 352;	Db	1 MDYQVSSPIYDINYTTSEPCOKINVQIAAR 31
Best Local Similarity	100.0%	Pred. No. 1.7e-16;		
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy . 1 MDYQVSSPIYDINYTTSEPCOKINVQIAAR 31				RESULT 14
Db AAG80111 standard; protein; 352 AA.				AEE04321
XX ID AAG80111				ID AAE04321 standard; protein; 352 AA.
AC AAG80111;				XX XX
XX DT 17-JAN-2002 (first entry)				AC AAE04321;
DE Human CCR5 protein.				XX
XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;				XX
XX inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;				XX
XX chronic bowel inflammation; rheumatoid arthritis; cytostatic;				XX
XX antiinflammatory; antiasthmatic; immunosuppressive; dermatological;				XX
XX antirheumatic; antiarthritic.				XX
OS Homo sapiens.				OS Homo sapiens.
XX US6258527-B1.				XX OS
PN WO200172830-A2.				PN PN
XX PD -				XX PD
XX PD - 04-OCT-2001.				XX 10-JUL-2001.
XX PF 02-APR-2001; 20001WO-EP003708.				XX PF
XX PT 31-MAR-2000; 20000DE-01016013.				XX PR
XX PA (IPFP-) IPF PHARM GMBH.				XX PR
PA (FORS-) FORSSMANN U.				XX DR
XX PI Forssmann W, Adermann K, Heitland F, Spodsborg N;				XX DR
XX DR; 2001-62625672.				XX N-PSDB; AAD08577.
XX Disclosure; Col 47-50; 37pp; English.				XX
XX PS Disclosure; Col 47-50; 37pp; English.				XX
CC The present invention relates to a transformed mammalian cell that contains a gene encoding CD4, a construct encoding a reporter gene under CC the regulation of an human immuno deficiency virus (HIV) long terminal CC repeat (LTR) and that has been transduced with a vector encoding a human CC chemokine receptor (CCR) where the CD4 and the CCR are present on the CC cell surface of transformed mammalian cell. The invention is useful for CC identifying drugs or antibodies that interfere with the translocation of CC HIV into transformed mammalian cell or for identifying a human chemokine CC receptor that facilitates the infection of a particular HIV strain into CC the transformed mammalian cell. Compounds identified can be used to treat CC cellular dysfunction and to prevent or combat HIV infection. The present CC sequence is a human chemokine receptor (CCR), CC-CCR5 related protein. CC CC-CCR5 is the principal cofactor for entry mediated by the envelope CC glycoproteins of primary macrophage-tropic strains of HIV-1				CC
CC Sequence 352 AA;				CC
CC Query Match 100.0%; Score 164; DB 4; Length 352;				CC
CC Best Local Similarity 100.0%; Pred. No. 1.7e-16;				CC
CC Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				CC
Qy 1 MDYQVSSPIYDINYTTSEPCOKINVQIAAR 31				Db
Db 1 MDYQVSSPIYDINYTTSEPCOKINVQIAAR 31				RESULT 15
Sequence 352 AA;				AEE07039

ID	AAE07039	standard; protein;	352 AA.	Qy	1 MDYQVSSPIYDINYTSEPCOKINVRCQAAR 31
XX	AAE07039;			Db	1 MDYQVSSPIYDINYTSEPCOKINVRCQAAR 31
AC					
XX					
DT	16-OCT-2001	(first entry)		Search completed:	July 29, 2004, 13:28:33
XX				Job time :	53 secs
DE	Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.				
XX					
KW	Human; G-protein Chemokine receptor; CCR5; HDGNR10; inflammation; HIV;				
KW	human immunodeficiency virus; antimicrobial; vasodilator; vulnerability;				
KW	cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;				
KW	neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;				
KW	rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;				
KW	gastrointestinal tract; lung; liver; immune disorder; Addison's disease;				
KW	haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;				
KW	multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;				
KW	cardiovascular disorder; myocardial ischaemia.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200158915-A2.				
XX					
PD	16-AUG-2001.				
XX					
PF	09-FEB-2001; 2001WO-US004152.				
XX					
PR	09-FEB-2000; 2000US-0181258P.				
PR	05-MAR-2000; 2000US-017999P.				
PR	22-SEP-2000; 2000US-0234336P.				
XX					
PA	(HUMA-) HUMAN GENOME SCI INC.				
XX					
PI	Rosen CA, Roschke V, Li Y, Ruben SM;				
XX					
DR	WPI; 2001-488965/53.				
DR	N-PSDB; AAD13198.				
XX					
PT	Isolated nucleic acid encoding a human G-protein chemokine receptor				
PT	- (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune				
PT	diseases e.g. rheumatoid arthritis, hyperproliferative disorders and				
PT	neurodegenerative disorders.				
XX					
PS	Example 40; Page 486-487; 495PP; English.				
XX					
CC	The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10				
CC	protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or				
CC	ameliorating a disease or disorder associated with inflammation,				
CC	defective or aberrant chemotaxis of immune cells, HIV infection (such as				
CC	Pneumocystis carinii pneumonia or Kaposi's sarcoma), or defective or				
CC	aberrant T-cell antigen presenting cell interaction. The disease or				
CC	disorder may also be an infectious disease (e.g. a viral infection such				
CC	as an early stage HIV infection, a cytomegalovirus infection, or a				
CC	poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or				
CC	a neurodegenerative disorder. The disease or disorder may be associated				
CC	with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5				
CC	ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein				
CC	is used as a food additive or preservative to increase or decrease				
CC	storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome				
CC	identification, and in gene therapy. CCR5 HDGNR10 DNA, protein,				
CC	antibodies, agonists and antagonists are also useful in the diagnosis,				
CC	treatment and prevention of cancer (breast, ovary, adrenal gland, bone,				
CC	bone marrow, gastrointestinal tract, liver, lung, urogenital); immune				
CC	disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,				
CC	autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple				
CC	sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular				
CC	disorders (myocardial ischaemias) and wound healing				
XX					
SQ	Sequence 352 AA;				
Query Match	100.0%	Score	164;	DB	4; Length 352;
Best Local Similarity	100.0%	Pred.	No. 1.7e-16;		
Matches	31;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:26:01 ; Search time 16 Seconds
(without alignments)
186.371 Million cell updates/sec

Title: US-09-852-238A-5
Perfect score: 164
Sequence: 1 MDYQSSPIIDNYXTSEPCOKINVQIAAR 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : PIR:78:*

1: pir1:
2: pir2:
3: pir3:
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	164	100.0	352	chemokine (C-C)-receptor 5 - human
2	57	34.8	178	hypothetical protein
3	54.5	33.2	130	actin depolymeriz
4	54	32.9	54	protein-tyrosine k
5	54	32.9	211	uracil phosphobi
6	54	32.9	617	5-methyltetrahydro
7	54	32.9	617	actin depolymeriz
8	53.5	32.6	132	conserved hypoth
9	53	32.3	516	E2 glycoprotein pr
10	52	31.7	1162	hypothetical prote
11	51.5	31.4	818	probable exported
12	51	31.1	364	E2 glycoprotein -
13	51	31.1	520	E2 glycoprotein pr
14	51	31.1	520	E2 glycoprotein pr
15	51	31.1	520	E2 glycoprotein -
16	51	31.1	544	laminin beta-1 cha
17	51	31.1	550	hypothetical prote
18	51	31.1	1130	protein F59810.1 l
19	51	31.1	1154	chemokine (C-C) re
20	51	31.1	1162	chemokine (C-C) re
21	51	31.1	1162	actin depolymerizi
22	51	31.1	1270	actin depolymerizi
23	49.5	30.2	1039	hypothetical prote
24	49	30.2	1192	alpha-mannosidase
25	49	29.9	360	E2 glycoprotein pr
26	49	29.9	374	E2 glycoprotein pr
27	48.5	29.6	126	E2 glycoprotein pr
28	48.5	29.6	130	E2 glycoprotein pr
29	48.5	29.6	141	E2 glycoprotein pr

ALIGNMENTS

RESULT 1									
A43113	Chemokine (C-C) receptor 5 - human	N;Alternate names: C-C CKR-5; CCR5							
	Hom sapiens (man)	C;Species: Homo sapiens (man)							
	C;Accession: A43113; S71808; A58834; A58832; G02653; A58833	C;Date: 12-Jul-1995 #sequence revision 12-Jul-1996 #text Change 20-Jun-2000							
R;Sanson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.	R;Sanson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.	R;Title: Resistance to HTLV-1 infection in caucasian individuals bearing mutant alleles of							
A;Reference number: S71808; MUID:96345670; PMID:8751444	A;Accession: S71808	A;Status: nucleic acid sequence not shown; not compared with conceptual translation							
A;Molecule type: DNA	A;Molecule type: DNA	A;Residues: 1-352 <SAM1>							
A;Cross-References: GB:X914942; NID:91262810; PID:CAA62796.1; PMID:91262811	A;Cross-References: GB:X914942; NID:91262810; PID:CAA62796.1; PMID:91262811	A;Molecule type: DNA							
R;Sanson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti, M.; Imai, T.; Rana, S.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pai, Nature 382, 722-725, 1996.	R;Sanson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti, M.; Imai, T.; Rana, S.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pai, Nature 382, 722-725, 1996.	A;Cross-References: GB:X59393; NID:91524062; PID:CAA67767.1; PMID:91524063							
A;Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to Yersinia plague infection	A;Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to Yersinia plague infection	R;Combaudiere, C.; Ahua, S.K.; Tiffany, H.L.; Murphy, P.M.							
J. Leukoc. Biol. 60, 147-152, 1996	J. Leukoc. Biol. 60, 147-152, 1996	J;Leukoc. Biol., 60, 147-152, 1996							
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor 5	A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor 5	A;Reference number: A58832; MUID:96295970; PMID:8699119							
A;Accession: A58832	A;Accession: A58832	A;Molecule type: mRNA							
A;Residues: 1-352 <CM1>	A;Residues: 1-352 <CM1>	A;Cross-References: GB:U57840; NID:91502408; PID:AB17071.1; PMID:91502409							
A;Status: translated from GB:EMBL/DBBJ	A;Status: translated from GB:EMBL/DBBJ	A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes							
A;Molecule type: mRNA	A;Molecule type: mRNA	A;Cross-References: EMBL:U57840							
A;Residues: 1-83, 'L', 91-352 <CM2>	A;Residues: 1-83, 'L', 91-352 <CM2>	A;Cross-References: C;Combadiere, C.							
R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.	R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.	R;Leukoc. Biol., 60, 147-152, 1996							
A;Title: Molecular cloning and functional characterization of a novel human CC chemokine A;Reference number: A58833; MUID:96291862; PMID:8663314	A;Title: Molecular cloning and functional characterization of a novel human CC chemokine A;Reference number: A58833; MUID:96291862; PMID:8663314	A;Title: Molecular cloning and functional characterization of a novel human CC chemokine A;Reference number: A58833; MUID:96291862; PMID:8663314							

A;Accession: A58833
A;Molecule type: mRNA
A;Residues: 1-352
A;Cross-references: GB:U54994; NID:91457945; PIDN: AAC50598.1; PID:gi1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30575). It binds to a complex of chemokine and dual-tropic strains of HIV-1.
C;Genetics:
A;Gene: GDB:CMKBR5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDR:1230510; OMIM:601373
A;Map position: 3p21.3p21
C;Function:
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES. Probably acts to control granulocyte proliferation and differentiation.
C;Superfamily: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
E:12-56-/Domain: transmembrane #status predicted <TM1>
E:12-87-/Domain: transmembrane #status predicted <TM2>
E:103-124-/Domain: transmembrane #status predicted <TM3>
E:142-166-/Domain: transmembrane #status predicted <TM4>
E:193-218-/Domain: transmembrane #status predicted <TM5>
E:236-257-/Domain: transmembrane #status predicted <TM6>
E:285-300-/Domain: transmembrane #status predicted <TM7>
F:268-/Binding site: carbohydrate (#status predicted)
F:336-337-/Binding site: phosphate (Ser) (covalent) #status predicted
F:340-343-/Binding site: phosphate (Thr) (covalent) #status predicted

Query	Match	Score	Length	Pred.	No.	Gaps
		100.0%	352			
		Best Local Similarity	100.0%	Pred. No.	8.4e-16	
Matches	31	Conservative	0	Mismatches	0	Gaps
				Indels	0	

"
Dy 1 MDYQVSSPIVDINYTTSEPCOKINVQIAAR 31
Db 1 MDYQVSSPIVDINYTTSEPCOKINVQIAAR 31

RESULT 2

T20317

Cryptothecical protein D1081.6 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*
C;Accession: T20317
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R;Dobson, R.
A;Reference number: Z19256
A;Accession: T20317
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-178 <WIL>
A;Cross-references: EMBL:Z75710; PIDN: CAB00027.1; GSPDB: GN00019; CESP:D1081.6
A;Experimental source: clone D1081
C;Genetics:
A;Gene: CESP:D1081.6
A;Map position: 1
A;Introns: 95/3; 114/3

Query	Match	Score	Length	Pred.	No.	Gaps
		34.8%	178			
		Best Local Similarity	52.9%	Pred. No.	0.94	
Matches	9	Conservative	3	Mismatches	5	Gaps
				Indels	0	

Dy 3 YQVSSPIVDINYTTSEPC 19
Db 47 EQVQIPLDNYTVAPEP 63

RESULT 3

T47540

Actin depolymerizing factor 2 - *Arabidopsis thaliana*

C;Alternate names: Protein F16L2.210
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Accession: T47540
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
R;Jordan, N.; Bangerl, S.; Wiedemann, R.; Voss, H.; Unseld, M.; Newes, H.W.; Rudd, S.

RESULT 8
G8717
 Query Match Score 54; DB 2; Length 211;
 Best Local Similarity 45.5%; Pred. No. 3.1;
 Matches 15; Conservative 4; Mismatches 10; Indels 4; Gaps 2;
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C;Accession: G84717
 R;Lin, X.; Kaul, S.; Rounslay, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Liu, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Saarberg, S.L.; Fraser, C.M.; Venter, J.; Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:1067197
 A;Accession: G84717
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-132 <STOP>
 A;Cross-references: GB:AE02093; PIDN:94432815; NID:94432815; PIDN:AAD20665.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g31200
 A;Map position: 2
 C;Superfamily: cofillin

Query Match Score 53.5%; DB 2; Length 132;
 Best Local Similarity 35.5%; Pred. No. 2.2;
 Matches 11; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 C;Accession: T40181
 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.; submitted to the EMBL Data Library, February 1998
 A;Reference number: 221910
 A;Status: Preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Cross references: EMBL:297992; PIDN:CAB10810.1; GSPDB:GN00067; SPDB:SPBC30D10.15
 A;Experimental source: strain 972h-; cosmid c30D10
 C;Genetics:
 A;Gene: SPDB:SPBC30D10.15
 A;Map position: 2

Query Match Score 53%; DB 2; Length 516;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 C;Accession: T40181
 R;Sutou, S.; Seto, S.; Okabe, T.; Nakai, M.; Sasaki, N.
 A;Title: Cloning and sequencing of genes encoding structural proteins of avian infectious virology 165, 589-595, 1988
 A;Reference number: A29249; MUID:88306251; PMID:2841803
 A;Accession: B2249
 A;Molecule type: genomic RNA

RESULT 6
AF1284
 5-methyltetrahydrofolate-homocysteine methyltransferase (methH) homolog lmo1678 [imported]
 C;Species: Listeria monocytogenes
 C;Accession: AF1284
 R;Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baguero, F.; Berche, P.; Bloecher, R.; Domínguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.; D.J. Jones, L.M.; Karst, U.; Science 294, 849-852, 2001
 A;Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A;Title: Comparative genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537219; PMID:11679669
 A;Accession: AF1284
 A;Experimental source: GB:NC_003210; PIDN:GAC99756.1; PID:91641114; GSPDB:GN00177
 A;Residues: 1-617 <GLA>
 A;Cross-references: GB:NC_003210; PIDN:GAC99756.1; PID:91641114; GSPDB:GN00177
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: lmo1678

Query Match Score 54; DB 2; Length 617;
 Best Local Similarity 42.3%; Pred. No. 10;
 Matches 11; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
 C;Accession: AF1284
 R;Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baguero, F.; Berche, P.; Bloecher, R.; Domínguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.; D.J. Jones, L.M.; Karst, U.; Science 294, 849-852, 2001
 A;Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A;Title: Comparative genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537219; PMID:11679669
 A;Accession: AF1284
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-617 <GLA>
 A;Cross-references: GB:AF1284; PIDN:GAC97017.1; PID:916414273; GSPDB:GN00178
 A;Experimental source: strain Clip11262
 C;Genetics:
 A;Gene: lmo1788

Query Match Score 54; DB 2; Length 617;
 Best Local Similarity 42.3%; Pred. No. 10;
 Matches 11; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
 C;Accession: B29249
 R;Sutou, S.; Seto, S.; Okabe, T.; Nakai, M.; Sasaki, N.
 A;Title: Cloning and sequencing of genes encoding structural proteins of avian infectious virology 165, 589-595, 1988
 A;Reference number: A29249; MUID:88306251; PMID:2841803
 A;Accession: B2249
 A;Molecule type: genomic RNA

RESULT 7
AI1655
 5-methyltetrahydrofolate-homocysteine methyltransferase (methH) homolog lin1786 [imported]
 C;Species: Listeria innocua
 C;Accession: AI1655
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baguero, F.; Berche, P.; Bloecher, R.; Domínguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.; D.J. Jones, L.M.; Karst, U.; Science 294, 849-852, 2001
 A;Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A;Title: Comparative genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537219; PMID:11679669
 A;Accession: AI1655
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-617 <GLA>
 A;Cross-references: GB:AI1655; PIDN:GAC97017.1; PID:916414273; GSPDB:GN00178
 A;Experimental source: strain Clip11262
 C;Genetics:
 A;Gene: lin1788

Query Match Score 54; DB 2; Length 617;
 Best Local Similarity 42.3%; Pred. No. 10;
 Matches 11; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
 C;Accession: B29249
 R;Sutou, S.; Seto, S.; Okabe, T.; Nakai, M.; Sasaki, N.
 A;Title: Cloning and sequencing of genes encoding structural proteins of avian infectious virology 165, 589-595, 1988
 A;Reference number: A29249; MUID:88306251; PMID:2841803
 A;Accession: B2249
 A;Molecule type: genomic RNA

RESULT 8
G8717
 actin depolymerizing factor 6 [imported] - *Arabidopsis thaliana*
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C;Accession: G84717
 R;Lin, X.; Kaul, S.; Rounslay, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Liu, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Saarberg, S.L.; Fraser, C.M.; Venter, J.; Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:1067197
 A;Accession: G84717
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-132 <STOP>
 A;Cross-references: GB:AE02093; PIDN:94432815; NID:94432815; PIDN:AAD20665.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g31200
 A;Map position: 2
 C;Superfamily: cofillin

Query Match Score 53.5%; DB 2; Length 132;
 Best Local Similarity 35.5%; Pred. No. 2.2;
 Matches 11; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 C;Accession: T40181
 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.; submitted to the EMBL Data Library, February 1998
 A;Reference number: 221910
 A;Status: Preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Cross references: EMBL:297992; PIDN:CAB10810.1; GSPDB:GN00067; SPDB:SPBC30D10.15
 A;Experimental source: strain 972h-; cosmid c30D10
 C;Genetics:
 A;Gene: SPDB:SPBC30D10.15
 A;Map position: 2

Query Match Score 53%; DB 2; Length 516;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 C;Accession: T40181
 R;Sutou, S.; Seto, S.; Okabe, T.; Nakai, M.; Sasaki, N.
 A;Title: Cloning and sequencing of genes encoding structural proteins of avian infectious virology 165, 589-595, 1988
 A;Reference number: A29249; MUID:88306251; PMID:2841803
 A;Accession: B2249
 A;Molecule type: genomic RNA

A;Residues: 1-1162 <SUT>
A;Cross-references: GB:M21515; PIDN:AAA66578.1; PID:9331187
C;KeyWords: Glycoprotein; spike protein
P;1-18/Domain: signal sequence predicted <SIG>
P;19-537/Product: E2 glycoprotein subunit S1 #status Predicted <GS1>
P;538-1162/Product: E2 glycoprotein subunit S2 #status Predicted <GS2>
P;51,77,103/144,163,178,212,237,247,264,271,276,283,306,425,447,513,530,579,591,669,676,
Query Match Score 52; DB 1; Length 1162;
Best Local Similarity 31.7%;
Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
Qy 1 MDYQVSSPIYDINYTSEPCQKIN 24
Db 472 IDIFVVOQSBYGLNYKVNFCEDVN 495

RESULT 11
T40491 hypothetical protein SPBC4C3.06 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40491
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Iauber, J.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, February 1998
A;Reference number: 231910
A;Accession: T40491
A;Status: preliminary; translated from GB/EMBL/DDBU
A;Molecule type: DNA
A;Cross-references: EMBL:AL021730; PIDN:CAA16828.1; SPDB:SPBC4C3.06
A;Experimental source: strain 972h-; cosmid C4C3
C;Genetics:
A;Gene: SPDB:SPBC4C3.06
A;Map position: 2
A;Introns: 14/3

Query Match Score 31.4%;
Best Local Similarity 40.0%;
Matches 12; Conservative 8; Mismatches 7; Indels 3; Gaps 2;
Qy 4 QVSSPIYD--INYYTSEPCQKINVKQIAAR 31
Db 99 QIASQVYKPLIDYTYTSSP-QTATLRRRAER 127

RESULT 12
AE0169 probable exported protein YPO1387 [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AE0169
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; M.; Rutherdorf, K.; Simmonds, M.; Skellon, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature, 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Accession: AE0169
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-364 <KUR>
A;Cross-references: GB:AL590842; PIDN:CA90216.1; PIDN:915979436; GSDB:GN00175
C;Genetics:
A;Gene: YPO1387

Query Match Score 31.1%;
Best Local Similarity 50.0%;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MDYQVSSPIYDINYTSE 18
Db 1 :||| :||| :||| :||| :

RESULT 13
S14559 avian infectious bronchitis virus (strain UK/142/86) (fragment)
E2 glycoprotein - avian infectious bronchitis virus
N;Alternate names: spike Glycoprotein chain S1
C;Species: avian infectious bronchitis virus, IBV
A;Variety: strain UK/142/86
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 20-Sep-1999
C;Accession: S14559
R;Cavanagh, D.; Davis, P.J.; Cook, J.K.A.; Li, D.; Kant, A.; Koch, G.
submitted to the EMBL Data Library, March 1991
A;Description: Infectious bronchitis virus: the S1 spike glycoprotein subunits of some strains of avian infectious bronchitis virus
A;Reference number: S14559
A;Accession: S14559
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-520 <CAV>
C;Cross-references: EMBL:X58066; PID:959027; PIDN:CAA41097.1; PID:959028
C;Superfamily: coronavirus E2 glycoprotein
Query Match Score 31.1%;
Best Local Similarity 46.7%;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 10 YDINYTTSEPCQKIN 24
Db 464 YGLNNYYKVNPCEDVN 478

RESULT 14
S14600 avian infectious bronchitis virus (strain UK/123/82) (fragment)
E2 glycoprotein precursor - avian infectious bronchitis virus
N;Alternate names: spike glycoprotein chain S1
C;Species: avian infectious bronchitis virus, IBV
A;Variety: strain UK/123/82
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 20-Sep-1999
C;Accession: S14600
R;Cavanagh, D.; Davis, P.J.; Cook, J.K.A.; Li, D.; Kant, A.; Koch, G.
submitted to the EMBL Data Library, March 1991
A;Description: Infectious bronchitis virus: the S1 spike glycoprotein subunits of some strains of avian infectious bronchitis virus
A;Reference number: S14558
A;Accession: S14600
A;Molecule type: genomic RNA
A;Residues: 1-320 <CAV>
C;Cross-references: EMBL:X58067; PID:959029; PIDN:CAA41098.1; PID:959030
C;Superfamily: coronavirus E2 glycoprotein
C;Species: avian infectious bronchitis virus
P;1-520/Product: E2 glycoprotein; prelomer protein; spike protein
F;5,14,12,127,146,161,195,220,247,254,259,285,408,430,496,513/Binding site: carboxy
Query Match Score 31.1%;
Best Local Similarity 46.7%;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 10 YDINYTTSEPCQKIN 24
Db 464 YGLNNYYKVNPCEDVN 478

RESULT 15
S14598 avian infectious bronchitis virus (strain UK/167/84)
E2 glycoprotein - avian infectious bronchitis virus
N;Alternate names: spike Glycoprotein chain S1
C;Species: avian infectious bronchitis virus, IBV
A;Variety: strain UK/167/84
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C;Accession: S14598
R;Cavanagh, D.; Davis, P.J.; Cook, J.K.A.; Li, D.; Kant, A.; Koch, G.
submitted to the EMBL Data Library, March 1991
A;Description: Infectious bronchitis virus: the S1 spike glycoprotein subunits of some strains of avian infectious bronchitis virus
A;Reference number: S14598

A;Accession: S14598
A;Stratus: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-520 <CAV>
A;Cross-references: EMBL:X58065; NID:959025; PID:CAA41096.1; PID:g59026
C;Superfamily: coronavirus E2 glycoprotein

Query Match 31.1%; Score 51; DB 2; Length 520;
Best Local Similarity 46.7%; Pred. No. 22;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy	10	YDINYTTSEPKQKIN	24
	464	YGINYYKVNFCEDVN	478

Search completed: July 29, 2004, 13:30:11
Job time : 17 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:24:41 ; Search time 14 Seconds
(without alignments)
115.298 Million cell updates/sec

Title: US-09-852-238A-5
Perfect score: 164
Sequence: 1 MDYQVSSPIYDINYTYTSEPCQKINVQQTAAAR 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 141691 seqs, 5207055 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	164	100.0	352	1	CKR5_HUMAN	P1681	homo sapien
2	97.0	352	1	CKR5_PANTHER	P56440	pan troglodytes	
3	93.9	352	1	CKR5_CEREPY	Q9Cv42	cercoptile	
4	93.9	352	1	CKR5_CERTYO	Q67433	cercocebus	
5	93.9	352	1	CKR5_HYLUSY	Q9nnc5	hylobates	
6	93.9	352	1	CKR5_MACMHD	P79436	macaca mulatta	
7	93.9	352	1	CKR5_PAPHEA	P56441	papio hamadryas	
8	93.9	352	1	CKR5_PONPY	Q97881	pongo pygmaeus	
9	93.3	352	1	CKR5_PYGIBI	Q97882	pygathrix hoyi	
10	93.3	352	1	CKR5_PYGNAE	Q97887	trachypithecus	
11	93.3	352	1	CKR5_TRAFNE	Q97879	trachypithecus	
12	93.3	352	1	CKR5_TRAPAH	P56433	gorilla gorilla	
13	90.9	352	1	CKR5_HYMLG	Q9nnc9	hylobates macrorhinos	
14	89.6	352	1	CKR5_HYLML	P55493	cercoptile	
15	88.4	352	1	CKR5_CERAE	Q97883	hylobates lar	
16	87.8	352	1	CKR5_HYLLE	P51682	mus musculus	
17	105	64.0	354	1	CKR5_MOUSE	Q05556	rattus norvegicus
18	64.0	354	1	CKR5_RAT	P51683	mus musculus	
19	33.8	373	1	CKR2_MOUSE	Q55193	rattus norvegicus	
20	33.8	373	1	CKR2_RAT	Q39251	arribidopsis	
21	33.2	137	1	ADPF2_ARATH	Q9zak3	arabidopsis	
22	33.2	139	1	ADPF4_ARATH	Q9cc99	lactococcus	
23	32.9	211	1	UPP_LACLA	P50926	lactococcus	
24	32.9	211	1	UPP_LACLC	Q9Fv12	petunia hybrida	
25	32.6	139	1	ADPF1_ARATH	Q9zak2	arabidopsis	
26	32.6	146	1	ADPF6_ARATH	Q8bg3	vitis vinifera	
27	32.3	143	1	ADF_VITVI	P14310	schizosaccharomyces pombe	
28	32.3	156	1	YB4F_SCHPO	P12550	avian infection	
29	31.7	1162	1	VGL2_IBVU3	P11046	drosophila melanogaster	
30	31.7	1790	1	LMB1_BROME	Q39450	arabidopsis thaliana	
31	31.1	139	1	ADF1_ARATH	P30206	avian infection	
32	31.1	520	1	VGL2_IBVU1	P30207	avian infection	
33	31.1	520	1	VGL2_IBVU2	P30208	avian infection	

ALIGNMENTS

RESULT 1	CKR5_HUMAN	STANDARD;	PRT;	352 AA.
ID	CKR5_HUMAN			
AC	P51681	; O14692; O14693; O14694; O14695; O14696; O14697; O14698; O14699;		
AC	O14700	; O14701; O14702; O14703; O14704; O14705; O14706; O14707;		
AC	O14708	; O15538; Q9UPX4;		
DT	01-OCT-1996	(Rel. 34; Created)		
DT	01-OCT-1996	(Rel. 34; Last sequence update)		
DE	15-MAR-2004	(Rel. 43; Last annotation update)		
DE	HIV-1 fusion co-receptor 5 (C-C CKR-5) (CCR-5) (CC-CKR-5) (CCR5)			
GN	CCRS OR CMKBR5.			
OS	Homo sapiens (Human).			
OC	Mammalia; Butheroidea; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarhini; Hominidae; Homo. NCBI TaxID:9606;			
RN	[1]			
SEQUENCE FROM N.A.				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96211590; PubMed=8639485;			
RA	Samson M., Labbe O., Mollerere C., Vassart G., Parmentier M.; "Molecular cloning and functional expression of a new human CC-chemokine receptor gene." Biochemistry 35:3362-3367 (1996).			
RT				
RL	Biochemistry 35:3362-3367 (1996).			
RN	[2]			
SEQUENCE FROM N.A.				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96291862; PubMed=8663314;			
RA	Report C.J., Gosling J., Schwechert V.L., Gray P.W., Charo I.F.; "Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha."			
RT	J. Biol. Chem. 271:17161-17166 (1996).			
RN	[3]			
SEQUENCE FROM N.A.				
RP	SEQUENCE FROM N.A.			
RX	Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.; "Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and RANTES."			
RT	J. Leukoc. Biol. 60:147-152 (1996).			
RL	[4]			
SEQUENCE FROM N.A.				
RP	SEQUENCE FROM N.A.			
RA	McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gao L., La Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcelli B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinski K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.; "Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses;" J. Virol. 71:8642-8656 (1997).			
RA	Kutmann S.E., Platt E.J., Kozak S.L., Kabat D.; "Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses;" J. Virol. 71:8642-8656 (1997).			

RN	[6]	SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX	MEDLINE=98022612; PubMed=959654;	
RA	Zhang J., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,	
RA	Ho D.D.;	"HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RT	'ARTS Res. Hum. Retroviruses 13:1357-1366(1997).	
RL		
RN		
		SEQUENCE FROM N.A.
RX	MEDLINE=98049523; PubMed=9388201;	
RA	Mummidi S., Anuja S.S., McDaniel B.L., Anuja S.K.;	
RT	"The human CC chemokine receptor 5 (CCR5) gene: Multiple transcripts with 5'-end heterogeneity, dual promoter usage, and evidence for RT polymorphisms within the regulatory regions and noncoding exons.";	
RT		
RL	J. Biol. Chem. 272:30662-30671(1997).	
RN		
		SEQUENCE FROM N.A., AND VARIANT ARG-178.
RP	Magierowska M., Barre-Sinoussi F., Iessafras H., Theodorou I.,	
RA	Debre P.;	
RL	Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.	
RN		
		SEQUENCE FROM N.A.
RP	Kopatz S.A., Aronstam R.S., Sharma S.V.;	
RT	"CDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)." ;	
RL	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.	
RN		
		CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX	MEDLINE=96260017; PubMed=8649511;	
RA	Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhardt M.,	
RA	di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,	
RA	Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;	
RT	"Identification of a major co-receptor for primary isolates of HIV-1." ;	
RL	Nature 381:661-666(1996).	
RN		
		[11] CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX	MEDLINE=96260018; PubMed=8649512;	
RA	Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,	
RA	Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,	
RA	Paxton W.A.;	"HIV-1 entry into CD4+ cells is mediated by the chemokine receptor CC-CKR-5."
RT		
RL	Nature 381:667-673(1996).	
RN		
		[12] SULFATION.
RP	MEDLINE=991.89752; PubMed=10089882;	
RA	Parzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,	
RA	Gerard N.P., Gerard C., Sodroski J., Choe H.;	
RT	"Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1 entry";	
RT	Cell 96:667-676(1999).	
CC	"- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and rantes and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation. Acts as co receptor with CD4 for primary non-synctytium-inducing strains (NSI) (macrophage-tropic) of HIV-1 virus. It promotes Env-mediated fusion of the virus.	
CC		
CC	"- SUBCELLULAR LOCATION: Integral membrane protein.	
CC	"- TISSUE SPECIFICITY: Found in promyelocytic cells.	
CC	"- PTM: Sulfation contributes to the efficiency of HIV-1 entry, glycosylation. Belongs to family 1 of G-protein coupled receptors.	
CC		
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CC		
		CC SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC		
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		CC EXTRACELLULAR (POTENTIAL).
		CC 1 (POTENTIAL).
		CC CYTOPLASMIC (POTENTIAL).
		2 (POTENTIAL).
		EXTRACELLULAR (POTENTIAL).
		3 (POTENTIAL).

RL AIDS Res. Hum. Retroviruses 15:931-939 (1999).
 CC :- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.

CC -|- SUBCELLULAR LOCATION: Integral membrane protein.

CC CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC DR EMBL; AF035222; AAD44015_1;

CC DR InterPro; IPR00076; GPCR_Rhodpsn.

CC DR PFam; PF00001; 7tm_1_1;

CC DR PRINTS; PR00237; GPCR_RHODOPSN.

CC DR PROSITE; PS00237; G PROTEIN RECEPT_F1_1;

CC DR PROSITE; PS00262; G PROTEIN RECBP_F1_2;

CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

CC FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

CC FT DOMAIN 31 58 1 (POTENTIAL).

CC FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

CC FT DOMAIN 69 89 2 (POTENTIAL).

CC FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

CC FT DOMAIN 103 124 3 (POTENTIAL).

CC FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

CC FT DOMAIN 142 166 4 (POTENTIAL).

CC FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

CC FT DOMAIN 199 218 5 (POTENTIAL).

CC FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

CC FT DOMAIN 236 260 6 (POTENTIAL).

CC FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).

CC FT DOMAIN 278 301 7 (POTENTIAL).

CC FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).

CC FT DISULFID 101 178 BY SIMILARITY.

CC FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

CC FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

CC FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

CC SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCCC3DB0 CRC64;

CC Score 93.9%; Score 154; DB 1; Length 352;

CC Best Local Similarity 93.5%; Pred. No. 1.5e-14; Indels 0; Gaps 0;

CC Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CC 1 MDYQVSSPTPYDIDYITSEPCOKINVQIAAR 31

CC 1 MDYQVSSPTPYDIDYITSEPCOKINVQIAAR 31

CC RESULT 4 CERTO STANDARD PRT; 352 AA.

CC ID CERTO STANDARD PRT; 352 AA.

CC AC 062743; 062744; 062745; 062746;

CC DT 15-DEC-1998 (Rel. 37, Created)

CC DT 16-OCT-2001 (Rel. 37, Last sequence update)

CC C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).

CC GN CCR5 OR CMKBR5.

CC OS Cercopithecidae (Red-crowned mangabey) (Sooty mangabey).

CC OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

CC OC NCBI_TaxID:9531;

CC RN [1] SEQUENCE FROM N.A.

CC RC STRAIN=Isolate 079, 085, 087, and 089;

CC RX MEDLINE=98321159; PubMed=656999;

CC RA Chen Z., Gettie A., Ho D.D., Marx P.A.,

CC [1] SEQUENCE FROM N.A.

CC RC STRAIN=Isolate 079, 085, 087, and 089;

CC RX MEDLINE=98321159; PubMed=656999;

CC RA Chen Z., Gettie A., Ho D.D., Marx P.A.,

CC "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabey naturally infected in West Africa: a comparison of coreceptor usage of primary SIVsm, HIV-2, and SIVmac.";
 CC RT Virology 246:113-124 (1998).
 CC -|- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC or send an email to license@isb-sib.ch).

CC DR EMBL; AF051902; AAC39830_1;

CC DR EMBL; AF051903; AAC39831_1;

CC DR EMBL; AF051904; AAC39832_1;

CC DR EMBL; AF051905; AAC39833_1;

CC DR InterPro; IPR000276; GPCR_Rhodpsn.

CC DR PRINTS; PR00001; 7tm_1_1;

CC DR PROSITE; PS00237; G PROTEIN RECEP_F1_1;

CC DR PROSITE; PS00262; G PROTEIN RECEP_F1_2;

CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

CC DR FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

CC DR FT DOMAIN 31 58 1 (POTENTIAL).

CC DR FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

CC DR FT DOMAIN 69 89 2 (POTENTIAL).

CC DR FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

CC DR FT DOMAIN 103 124 3 (POTENTIAL).

CC DR FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

CC DR FT DOMAIN 142 166 4 (POTENTIAL).

CC DR FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

CC DR FT DOMAIN 199 218 5 (POTENTIAL).

CC DR FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

CC DR FT DOMAIN 236 260 6 (POTENTIAL).

CC DR FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).

CC DR FT DOMAIN 278 301 7 (POTENTIAL).

CC DR FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).

CC DR FT DISULFID 101 178 BY SIMILARITY.

CC DR FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 14 14 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

CC DR FT VARIANT 2 2 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 3 3 CYTOPLASMIC (POTENTIAL).

CC DR FT VARIANT 15 15 6 (POTENTIAL).

CC DR FT VARIANT 261 277 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 278 301 7 (POTENTIAL).

CC DR FT VARIANT 302 352 CYTOPLASMIC (POTENTIAL).

CC DR FT DISULFID 101 178 BY SIMILARITY.

CC DR FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 14 14 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

CC DR FT VARIANT 2 2 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 3 3 CYTOPLASMIC (POTENTIAL).

CC DR FT VARIANT 15 15 6 (POTENTIAL).

CC DR FT VARIANT 261 277 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 278 301 7 (POTENTIAL).

CC DR FT VARIANT 302 352 CYTOPLASMIC (POTENTIAL).

CC DR FT DISULFID 101 178 BY SIMILARITY.

CC DR FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 14 14 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

CC DR FT VARIANT 2 2 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 3 3 CYTOPLASMIC (POTENTIAL).

CC DR FT VARIANT 15 15 6 (POTENTIAL).

CC DR FT VARIANT 261 277 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 278 301 7 (POTENTIAL).

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CC DR FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 14 14 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

CC DR FT VARIANT 2 2 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 3 3 CYTOPLASMIC (POTENTIAL).

CC DR FT VARIANT 15 15 6 (POTENTIAL).

CC DR FT VARIANT 261 277 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 278 301 7 (POTENTIAL).

CC DR FT VARIANT 302 352 CYTOPLASMIC (POTENTIAL).

CC DR FT DISULFID 101 178 BY SIMILARITY.

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CC DR FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 14 14 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

CC DR FT VARIANT 2 2 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 3 3 CYTOPLASMIC (POTENTIAL).

CC DR FT VARIANT 15 15 6 (POTENTIAL).

CC DR FT VARIANT 261 277 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 278 301 7 (POTENTIAL).

CC DR FT VARIANT 302 352 CYTOPLASMIC (POTENTIAL).

CC DR FT DISULFID 101 178 BY SIMILARITY.

CC DR FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

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CC DR FT VARIANT 3 3 CYTOPLASMIC (POTENTIAL).

CC DR FT VARIANT 15 15 6 (POTENTIAL).

CC DR FT VARIANT 261 277 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 278 301 7 (POTENTIAL).

CC DR FT VARIANT 302 352 CYTOPLASMIC (POTENTIAL).

CC DR FT DISULFID 101 178 BY SIMILARITY.

CC DR FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 14 14 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

CC DR FT VARIANT 2 2 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 3 3 CYTOPLASMIC (POTENTIAL).

CC DR FT VARIANT 15 15 6 (POTENTIAL).

CC DR FT VARIANT 261 277 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 278 301 7 (POTENTIAL).

CC DR FT VARIANT 302 352 CYTOPLASMIC (POTENTIAL).

CC DR FT DISULFID 101 178 BY SIMILARITY.

CC DR FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 14 14 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

CC DR FT VARIANT 2 2 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 3 3 CYTOPLASMIC (POTENTIAL).

CC DR FT VARIANT 15 15 6 (POTENTIAL).

CC DR FT VARIANT 261 277 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 278 301 7 (POTENTIAL).

CC DR FT VARIANT 302 352 CYTOPLASMIC (POTENTIAL).

CC DR FT DISULFID 101 178 BY SIMILARITY.

CC DR FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 14 14 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

CC DR FT VARIANT 2 2 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 3 3 CYTOPLASMIC (POTENTIAL).

CC DR FT VARIANT 15 15 6 (POTENTIAL).

CC DR FT VARIANT 261 277 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 278 301 7 (POTENTIAL).

CC DR FT VARIANT 302 352 CYTOPLASMIC (POTENTIAL).

CC DR FT DISULFID 101 178 BY SIMILARITY.

CC DR FT MOD_RES 3 3 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 10 10 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 14 14 SULFATION (BY SIMILARITY).

CC DR FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

CC DR FT VARIANT 2 2 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 3 3 CYTOPLASMIC (POTENTIAL).

CC DR FT VARIANT 15 15 6 (POTENTIAL).

CC DR FT VARIANT 261 277 EXTRACELLULAR (POTENTIAL).

CC DR FT VARIANT 278 301 7 (POTENTIAL).

CC DR FT VARIANT 302 352 CYTOPLASMIC (POTENTIAL).

CC DR FT DISULFID 101 178 BY SIMILARITY.

15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 DB CCR5 OR CMKBR5.
 GN OS Hylobates syndactylus ("Siamang") (Symphalangus syndactylus).
 OC OC Bukayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9590;
 RN [1]
 RP SEQUENCE FROM N.A.; PubMed=10486970;
 RA Zhang Y.-W., Ryter O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154 (1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MCP-1-alpha,
 CC MCP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC DR EMLB:AF177884; AAK43367.1; -;
 CC DR * InterPro:IPR000276; GPCR_Rhodopsin.
 CC DR PRINTS: PR00237; GPROTEIN_RECEP_F1_1; 1.
 CC DR PROSITE: PS000237; G-PROTEIN_RECEP_F1_2; 1.
 CC DR PROSITE; PS050262; G-PROTEIN_RECEP_F1_3; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 5 (POTENTIAL).
 FT TRANSMEM 199 219 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 219 235 6 (POTENTIAL).
 FT TRANSMEM 236 260 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 261 277 7 (POTENTIAL).
 FT TRANSMEM 278 301 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 302 352 BY SIMILARITY.
 FT MOD_RES 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40508 MW; F4F6B3ADAF658A CR664;

Query Match 93.9%; Score 154; DB 1; Length 352;
 Best Local Similarity 93.5%; Pred. No. 1.5e-14;
 Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSYYDINYTTSEPCQXINVQIAAR 31
 ID CKR5_MACMU STANDARD;
 AC P79436; 002746;
 Db 1 MDYQVSSYYDYYTSEPCQXINVQIAAR 31
 DT 01-NOV-1997 (Rel. 35, Created)

RESULT 6
 CKR5_MACMU
 ID CKR5_MACMU STANDARD;
 AC P79436; 002746;
 DT 01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 DB CCR5 OR CMKBR5.
 GN Macaca mulatta (Rhesus macaque),
 OS Macaca mulatta (Crab eating macaque) (Cynomolgus monkey), and
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544; 9541; 9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta; STRAIN=Indian macaque;
 RX MEDLINE=97184599; PubMed=9032394;
 RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
 RA Newman W., Gerard N., Gerard C., Sodroski J.;
 RT "Utilization of C-C chemokine receptor 5 by the envelope glycoproteins of a pathogenic simian immunodeficiency virus, SIVmac239";
 RT J. Virol. 71:2522-2527(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta; STRAIN=Indian macaque;
 RX MEDLINE=97184599; PubMed=9032394;
 RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
 RT "Genetically divergent strains of simian immunodeficiency virus use CCR5 as a coreceptor for entry.;"
 RT J. Virol. 71:2705-2714(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta; STRAIN=Indian macaque;
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
 RX MEDLINE=97268687; PubMed=108095;
 RA Edinger A.L., Ameece A., Miller K., Doranz B.J., Endres M.,
 RA Sharron M., Sammon M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Pammentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains.;"
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC DR EMLB:U77672; AAC51109.1;
 CC DR EMBL:U73739; AAC51158.1;
 CC DR EMBL:U96762; AAC34132.1;
 CC DR EMBL:AF005660; AAB62554.1;
 CC DR EMBL:AF005661; AAB62555.1;
 CC DR EMBL:AF005662; AAB62556.1;
 CC DR InterPro: IPR00276; GPCR_Rhodopsin.
 CC DR Pfam; PF00001; 7em_1; 1.
 CC DR PRINTS; PR00237; G_PROTEIN_RECEP_F1_1.
 CC DR PROSITE; PS000237; G-PROTEIN_RECEP_F1_2.

Query Match 93.9%; Score 154; DB 1; Length 352;
 Best Local Similarity 93.5%; Pred. No. 1.5e-14;
 Matches 29; Conservative 1; Mismatches 1; Indels 0; Gap 0;
 Qy 1 MDYQVSSPIDIYNTSEPCOKINVQIAAR 31
 Db 1 MDYQVSSPIDIYNTSEPCOKINVQIAAR 31

RESULT 7

CRS_PAPHA	PAPHA	STANDARD:	PRT:	352 AA.
AC P56441;				
DT 15-JUL-1998	(Rel. 36, Created)			
DT 15-JUL-1998	(Rel. 36, Last sequence update)			
DT 16-OCT-2001	(Rel. 40, Last annotation update)			
GN CCR5 OR CMKBR5.	C-C chemokine receptor type 5 (C-C CCR-5) (CC-CCR-5) (CCR-5) (CCR5)			
OS Papio hamadryas	(Hamadryas baboon), and			
OS Papio anubis	(Olive baboon)			
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;				
OC Cercopithecinae; Papio.				
OX NCBI TaxID:955;				

SEQUENCE FROM N.A.
 SPECIES=P.hamadryas;
 MEDLINE=91286537; PubMed=9108095;
 Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 Sharpen M., Samson M., Lu Z.H., Clement J.E., Murphy-Corb M.,
 Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 "Differential utilization of CCR5 by macrophage and T cell tropic
 simian immunodeficiency virus strains";
 Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).

[2] SEQUENCE FROM N.A.
SPECIES=P hamadryas;
MEDLINE=9310133; PubMed=10195758;
Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.
"Species-specific changes in the CCR5 gene from African and Asian
nonhuman primates.";
AIDS Res. Hum. Retroviruses 15:479-483 (1999).

[3] SEQUENCE FROM N.A.
SPECIES=P anubis;
Benton P.A.; Timanus D.K.; Shearer M.H.; Lee D.R.; Kennedy R.C.;

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; AF005658; ARB62552; 1.
 CC DR EMBL; AF105287; AAD20556; 1.
 CC DR EMBL; AF105288; AAD20557; 1.
 CC DR EMBL; AF105289; AAD20558; 1.
 CC DR EMBL; AF105290; AAD20559; 1.
 CC DR EMBL; AF2023452; AAC63830; 1.
 CC DR InterPro; IPR00276; GPCR_Rhodopsin.
 CC DR Pfam; PF00001; 7m1; 1.
 CC DR PRINTS; PR00237; GPCR_RHODOPSIN.
 CC DR PROSITE; PS00237; G-PROTEIN_RBCEP_F1-1; 1.
 CC DR PROSITE; PS00262; G-PROTEIN_RBCEP_F1-2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 31 58 1 (POTENTIAL).
 CC FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 69 89 2 (POTENTIAL).
 CC FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 103 124 3 (POTENTIAL).
 CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 142 166 4 (POTENTIAL).
 CC FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 199 218 5 (POTENTIAL).
 CC FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 236 260 6 (POTENTIAL).
 CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 278 301 7 (POTENTIAL).
 CC FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 CC FT DISUFD 101 178 BY SIMILARITY.
 CC MOD_RES 3 3 SULFATION (BY SIMILARITY).
 CC MOD_RES 10 10 SULFATION (BY SIMILARITY).
 CC MOD_RES 14 14 SULFATION (BY SIMILARITY).
 CC MOD_RES 15 15 SULFATION (BY SIMILARITY).
 CC CAREBHYD 268 268 N-LINKED GLCNAC . (POTENTIAL).
 CC SEQUENCE 352 AA: 40489 MW: 5E1504A9BA1FE8B2 CRC64 ;

OX	NCBI_TaxID=9600;							
RN	[1]	SEQUENCE FROM N.A.						
RP	MEDLINE=99416438; PubMed=10486970;							
RX	Zhang Y.-W., Ryder O.A., Zhang Y.-P.; "Sequence evolution of the CCR5 chemokine receptor gene in primates.";							
RA	RT Mol. Biol. Evol. 16:1145-1154(1999).							
RT	"Sequence evolution of the CCR5 chemokine receptor gene in primates.";							
RL	Zhang Y.-W., Ryder O.A., Zhang Y.-P.; "Sequence evolution of the CCR5 chemokine receptor gene in primates.";							
CC	CC -!- MIP-1-alpha: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta, and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.							
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.							
CC	-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.							
CC	CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.							
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CC	CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.							
DR	EMBL; AF075446; AAD119858.1; -;							
DR	InterPro; IPR000276; GPCR_Rhodopsin.							
DR	PRINTS; PR00001; 7em_1; 1.							
DR	PFAM; PF00001; 7em_1; 1.							
DR	PROSITE; PS00237; GPROTRHODOPSIN.							
DR	PROSITE; PS00237; GPROTRHODOPSIN.							
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.							
FT	DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).							
FT	TRANSMEM 31 58 1 (POTENTIAL).							
FT	DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).							
FT	TRANSMEM 69 89 2 (POTENTIAL).							
FT	DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).							
FT	TRANSMEM 103 124 3 (POTENTIAL).							
FT	DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).							
FT	TRANSMEM 142 166 4 (POTENTIAL).							
FT	DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).							
FT	TRANSMEM 199 218 5 (POTENTIAL).							
FT	DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).							
FT	TRANSMEM 236 260 6 (POTENTIAL).							
FT	DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).							
FT	TRANSMEM 278 301 7 (POTENTIAL).							
FT	DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).							
FT	TRANSMEM 303 352 BY SIMILARITY.							
FT	MOD_RES 3 3 SULFATION (BY SIMILARITY).							
FT	MOD_RES 10 10 SULFATION (BY SIMILARITY).							
FT	MOD_RES 14 14 SULFATION (BY SIMILARITY).							
FT	MOD_RES 15 15 SULFATION (BY SIMILARITY).							
SQ	SEQUENCE 352 AA; 40527 MW; F4E2247135AF65BA CRC64;							
Query Match	93.9% Score 154; DB 1; Length 352;							
Best Local Similarity	93.5%; Pred. No. 1.5e-14;							
Matches 29	Conservative 1; Mismatches 1; Indels 0; Gaps 0;							
Qy	1 MDYQVSSPPYYDINYNTTSEPCOKINVQIAAR 31							
Db	1 MDYQVSSPPYYDINYNTTSEPCOKINVQIAAR 31							
RESULT 9								
CKR5_-PYGBI	STANDARD; PRT; 352 AA.							
ID	CKR5_PYGNE							
AC	O97880; 30-MAY-2000 (Rel. 39, Created)							
DT	30-MAY-2000 (Rel. 39, Last sequence update)							
DT	28-FEB-2003 (Rel. 41, Last annotation update)							
DE	C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS-5).							
GN	CKR5 OR CMKBR5.							
OS	Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Etherida; Primates; Catarrhini; Cercopithecidae; Colobinae;							
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC Pygathrix
 OC NCBI_TAXID=54133;
 OC RXN [1] _
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates."
 RL Mol. Biol. Evol. 16:1145-1154 (1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; AF075448; AAD19860.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECEP_F1_1; 1.
 DR PROSITE; PS5062; G-PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; TRANSMEMbrane; Glycoprotein; Sulfation.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40532 MW; FE4F998D3B3E61 CRC4;

Query Match 93.3%: Score 153; DB 1; Length 352;
 Best Local Similarity 90.3%; Prod. No. 2.1e-14;
 Matches 28; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Gaps 0;

Qy 1 MDYQVSSPYDINYNTSREPCOKINVKQIAAR 31
 Ds 1 MDYQVSSPYDINYNTSREPCOKINVKQIAAR 31

RESULT 11
 CKR5_TRAFR ID CKR5_TRAFR STANDARD; PRT; 352 AA.
 AC 097878; DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR5) (CC-CKR-5) (CCR5).
 GN CCR5 OR CMKB5. DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR5).
 OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC NCBI_TAXID=54180;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates."
 RL Mol. Biol. Evol. 16:1145-1154 (1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC or send an email to license@isb-sib.ch).

CC DR EMBL; AF075442; AAD19854.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECEP_F1_1; 1.
 DR PROSITE; PS5062; G-PROTEIN RECEP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; G-protein coupled receptor; Transmembrane.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;

Query Match 93.3%: Score 153; DB 1; Length 352;
 Best Local Similarity 90.3%; Prod. No. 2.1e-14;
 Matches 28; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDYQVSSPYDINYNTSREPCOKINVKQIAAR 31
 Ds 1 MDYQVSSPYDINYNTSREPCOKINVKQIAAR 31

RESULT 12
 CKR5_TRAFR ID CKR5_TRAFR STANDARD; PRT; 352 AA.
 AC 097879; DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR5) (CC-CKR-5) (CCR5).
 GN CCR5 OR CMKB5. DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR5).
 OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).

OS	Trachypithecus phayrei (Phayre's leaf monkey).
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Trachypithecus.
OC	Metazoa; Eutheria; Primates; Catarhinini; Cercopithecidae; Colobinae;
RN	NCBI_TaxID=51618;
RP	SEQUENCE FROM N.A.
RX	MEDLINE=9416438; PubMed=10486970;
RA	Zhang Y.-W.; Ryder O.A.; Zhang Y.-P.; Miller K.; Doranz B.J.; Endres M.; Edinger A.L.; Amdeo A.; Sharpen M.; Samson M.; Lu Z.H.; Clements J.E.; Murhey-Corb M., Mol. Biol. Evol. 16:145-154 (1999).
RL	"Sequence evolution of the CCR5 chemokine receptor gene in primates."
CC	- - FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC	MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role
CC	in the control of granulocytic lineage proliferation or differentiation.
CC	- - SUBCELLULAR LOCATION: Integral membrane protein.
CC	- - SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC	This SWISS-PROT entry is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	EMBL; AF075443; AAD19855.1;
DR	InterPro; IPR000276; GPCR_RhoGDSn.
DR	PRINTS; PRO00237; GPCR_RHOOPSN.
DR	- PROSITE; PS50262; G-PROTEIN_RECEP_F1.1;
KW	- G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT	DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 31 58 1 (POTENTIAL).
FT	DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 69 89 2 (POTENTIAL).
FT	DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 103 124 3 (POTENTIAL).
FT	DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 142 166 4 (POTENTIAL).
FT	DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 199 218 5 (POTENTIAL).
FT	DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 236 252 BY SIMILARITY.
FT	DISULFID 101 178 BY SIMILARITY.
FT	MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT	TRANSMEM 236 260 6 (POTENTIAL).
FT	DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 278 301 7 (POTENTIAL).
FT	DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT	DISULFID 101 178 BY SIMILARITY.
FT	MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT	MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT	MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ	SEQUENCE 352 AA; 40509 MW; 43667148D3A593BF CRC64;
Query Match	Score 153; DB 1; Length 352;
Best Local Similarity	90.3%; Pred. No. 2.1e-14;
Matches 28; Conservative	Indels 0; Gaps 0;
Qy	1 MDYQVSSPIVDINYTSBPCOKINVQIAAR 31
Db	1 MDYQVSSPIVDIYTTSBPCOKINVQIAAR 31
RESULT 13	
ID CKR5_GORGO	STANDARD;
AC P56439;	PRT; 352 AA.
DT 15-JUL-1998 (Rel. 36, Created)	
DT 15-JUL-1998 (Rel. 36, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DB C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).	(CCR-5) (CCR5).
Qy	1 MDYQVSSPIVDINYTSBPCOKINVQIAAR 31
Db	1 MDYQVSSPIVDIYTTSBPCOKINVQIAAR 31
RESULT 14	
CKR5_HYML	STANDARD;
ID CKR5_HYML	PRT; 352 AA.
AC Q95NG0;	
DT 15-MAR-2004 (Rel. 43, Created)	
Query Match	Score 149; DB 1; Length 352;
Best Local Similarity	90.3%; Pred. No. 8e-14;
Matches 28; Conservative	1; Mismatches 2; Indels 0; Gaps 0;

DT	15-MAR-2004 (Rel. 43, Last sequence update)	
DT	C-C chemokine receptor type 5 (C-C CKR-5) (CCR5)	(CCR5)
DE	C-C chemokine receptor type 5 (C-C CKR-5) (CCR5)	(CCR5)
GN	CCR5 OR CMKBR5.	
RA	Zhang Y.-W. Ryder O.A., Zhang Y.-P.;	
RT	"Sequence evolution of the CCR5 chemokine receptor gene in primates.";	
RL	Mol. Biol. Evol. 16:1145-1154 (1999).	
CC	-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,	
CC	MIP-1-beta and RANTES and subsequently transduces a signal by	
CC	increasing the intracellular calcium ions level. May play a role	
CC	in the control of granulocytic lineage proliferation or	
CC	differentiation.	
CC	-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; AF177899; AAK43382; 1;	
DR	InterPro; IPR000276; GPCR_Rhodpsn.	
DR	Pfam; PF00001; 7tm_1.	
DR	PRINTS; PR00237; GPCR_RHODPSN.	
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.	
DR	PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.	
KW	- G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.	
FT	DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 31 58 1 (POTENTIAL).	
FT	DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 69 89 2 (POTENTIAL).	
FT	DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 103 124 3 (POTENTIAL).	
FT	DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 142 166 4 (POTENTIAL).	
FT	DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 199 218 5 (POTENTIAL).	
FT	DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 236 260 6 (POTENTIAL).	
FT	DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 278 301 7 (POTENTIAL).	
FT	DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).	
FT	DISULFID 101 178 BY SIMILARITY.	
FT	MOD_RES 3 3 SULFATION (BY SIMILARITY).	
FT	MOD_RES 10 10 SULFATION (BY SIMILARITY).	
FT	MOD_RES 14 14 SULFATION (BY SIMILARITY).	
SQ	SEQUENCE 352 AA; 40436 MW; 9623CP98340CF2/4 CR64;	
Query Match	1 MDYQVSSSTYDINYNTSSPQCKINVQTAAR 31	Score 147; DB 1; Length 352;
Best Local Similarity	90.3%	Pred. No. 1.5e-11;
Matches	28; Conservative	Mismatches 2; Indels 0; Gaps 0;
Db	1 MDYQVSSSTYDINYNTSSPQCKINVQTAAR 31	
RESULT 15		
CKR5_CERAE	STANDARD;	PRT; 352 AA.
ID	P5493;	
AC	7F52E60C7B2C29A CRC64;	
DT	15-JUL-1998 (Rel. 36, Created)	
DT	15-JUL-1998 (Rel. 36, Last sequence update)	
Query Match	88.4%; Score 145; DB 1; Length 352;	
Query	352 AA;	40561 MW;
Sequence	352 AA;	3

Best Local Similarity 90.3%; Pred. No. 2.9e-13;
Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDQYSSPITYDINYNTSEPCQKINVKQTAAR 31
Db 1 ||||| | | | | : ||||| ||||| ||||| |||||
Db 1 MDQYSSPITYDINYNTSEPCQKINVKQTAAR 31

Search completed: July 29, 2004, 13:28:57
Job time : 15 secs

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Result No.	Query Score	Match Length	DB ID	Description
1	164	100.0	215	075303 homo sapien
2	159	97.0	352	Q95nc3 miopithecus
3	159	97.0	352	018771 pan troglod
4	159	97.0	352	018772 pan troglod
5	159	97.0	352	Q9tqx0 cercopithec
6	154	93.9	344	Q9tqrx cercopithec
7	154	93.9	344	077833 cercopithec
8	154	93.9	352	Q9tqsk1 cercopithec
9	154	93.9	352	Q95nc5 hylobates s
10	154	93.9	352	Q9tv48 cercopithec
11	154	93.9	352	Q9tv49 cercopithec
12	154	93.9	352	Q9xt76 cercopithec
13	154	93.9	352	018770 pan troglod
14	154	93.9	352	Q9tv44 cercopithec
15	154	93.9	352	097975 macaca arct
16	154	93.9	352	Q9xt12 cercopithec

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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:25:16 ; Search time 35 Seconds

Perfect score: 164
Sequence: 1 MDYQVSSPIYDINTYTSEPCQKTNVKQIAAR 31

Title: US-09-852-238A-5
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rabbit:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriaph:
17: sp_archeap:
* * * * *

RESULT 1
075303 ID 075303 PRELIMINARY;

AC 075303 PRT; 215 AA.

DT 01-NOV-1998 (TRIMBLrel. 08, Created)

DT 01-JUN-2003 (TRIMBLrel. 08, Last sequence update)

DE CC-chemokine receptor.

GN CCR-5.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

RN [1] NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RA Tse L., Ehrenberg P.K., Chang G., Michael N.L.;

RT "Genomic Organization and Functional Characterization of the Complete

RT Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-

RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF003962; AAC23944.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; P:receptor activity; IEA.

DR GO; GO:0001584; P:rhinopain-like receptor activity; IEA.

DR GO; GO:007186; P:G-protein coupled receptor protein signalin. . . ; IEA.

DR Interpro: IPRO00276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm ; 1.

DR PRINTS; PR00237; GPCR_RHODOPSN.

DR PROSITE; PS00231; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

RW Receptor.

SQ SEQUENCE: 215 AA; 23946 MW;

Query Match 100.0%; Score 164; DB 4;

Best Local Similarity 100.0%; Pred. No. 4.8e-16;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MDYQVSSPIYDINTYTSEPCQKTNVKQIAAR 31

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Db	1 MDYQVSSPIYDINYTTSEPCQKINKVQIAAR 31	DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1. DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
RESULT 2		
O95NC3	PRELIMINARY;	PRT; 352 AA.
AC .O95NC3;		
DT 01-DEC-2001 (TrEMBLrel. 19, Created)		
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE C-C chemokine receptor 5.		
OS Miopithecus talapoin (talapoin) (Cercopithecus talapoain).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;		
OC Cercopitheciniae; Miopithecus.		
OX NCBI_TaxID=36231;		
RN [1]		
RP SEQUENCE FROM N.A.		
RA Zhang Y., Ryder O.A., Zhang Y.;		
RT "Sequence comparison of the CCR5 gene in primates and primate phylogeny." ;		
RT Submitted (AUG-1999) to the TrEMBL/GenBank/DDBJ databases.		
EMBL: AF177886; AAK13369; 1.		
DR GO; GO:0016001; C:integral to membrane; IEA.		
DR GO; GO:0004872; F:receptor activity; IEA.		
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR GO; GO:0001786; P:G-protein coupled receptor protein signalin.		.. ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.		
PFam; PF000237; GPCR_RHODOPSN.		
PRINTS; PR000237; GPCR_RHODOPSN.		
DR PROSITE; PS50237; G_PROTEIN_RECEP_F1_1; 1.		
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.		
KW Receptor.		
SEQUENCE 352 AA; 40546 MW; 6464152F3B566AB5 CRC64;		
Query Match	97.0%	Score 159; DB 6; Length 352;
Best Local Similarity	96.8%	Pred. No. 4.e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy 1 MDYQVSSPIYDINYTTSEPCQKINKVQIAAR 31		
Db 1 MDYQVSSPIYDINYTTSEPCQKINKVQIAAR 31		
RESULT 3		
O18771	PRELIMINARY;	PRT; 352 AA.
AC O18771;		
DT 01-JAN-1998 (TrEMBLrel. 05, Created)		
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)		
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE CCR5 receptor (Fragment).		
GN Pan troglodytes (Chimpanzee).		
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.		
NCBI_TaxID=9598;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN_CbCCR5-142a;		
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B., Ho D.D.;		
RA AIDS Res. Hum. Retroviruses 0-0-(1997).		
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism." ;		
RL AIDS Res. Hum. Retroviruses 0-0-(1997).		
DR EMBL; AF011541; AAB65741; 1.		
DR GO; GO:0016021; C:integral to membrane; IEA.		
DR GO; GO:0004872; F:receptor activity; IEA.		
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR InterPro; IPR000276; GPCR_Rhodpsn.		
DR PRINTS; PR000237; GPCR_RHODOPSN.		
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.		
DR PROSITE; PS50237; G_PROTEIN_RECEP_F1_2; 1.		
KW Receptor.		
FT NON TER	352	Score 159; DB 6; Length 352;
SQ SEQUENCE 352 AA; 40598 MW; 39688FA7004C952F CRC64;		
Query Match	97.0%	Score 159; DB 6; Length 352;
Best Local Similarity	96.8%	Pred. No. 4.e-15;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Qy 1 MDYQVSSPIYDINYTTSEPCQKINKVQIAAR 31		
Db 1 MDYQVSSPIYDINYTTSEPCQKINKVQIAAR 31		
RESULT 5		
O18771	PRELIMINARY;	PRT; 352 AA.
AC O18771;		
DT 01-MAY-2000 (TrEMBLrel. 13, Created)		
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DE CC chemokine receptor 5.		
GN Cercopithecus aethiops (Green monkey) (Grivet).		
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;		
OC Cercopithecinae; Cercopithecus.		
NCBI_TaxID=9334;		
RN [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN_CbCCR5-142a;		
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B., Ho D.D.;		
RA AIDS Res. Hum. Retroviruses 0-0-(1997).		
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism." ;		
RL AIDS Res. Hum. Retroviruses 0-0-(1997).		
DR EMBL; AF011539; AAB65739; 1.		
DR GO; GO:0016021; C:integral to membrane; IEA.		
DR GO; GO:0004872; F:receptor activity; IEA.		
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.		
DR InterPro; IPR000276; GPCR_Rhodpsn.		
DR PRINTS; PR000237; GPCR_RHODOPSN.		
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.		
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.		

OS Cercopithecus aethiops (Green monkey) (Grivet). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; OC Cercopithecinae; Cercopithecus. OX NCBI_TaxID=9534; RN [1] RP .SEQUENCE FROM N.A. RA Hollkamp N., Baier M., Werner A.; RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases. DR EMBL; AF019379; ADD1639; 1.. GO; GO:0016021; C:integral to membrane; IEA. DR GO; GO:000472; F:receptor activity; IEA. DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA. DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA. DR InterPro; IPR00001; 7tm_1..1. DR Pfam; PF00001; 7tm_1..1. DR PRINTS; PR00237; GPCR_RHODPSN. DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1..1. DR PROSITE; PS50262; G_PROTEIN_RECPEP_F1_2..1. KW Receptor. SEQUENCE 352 AA; 40588 MW; OPI869D946668DBB CRC64; SQ Query Match 93.9%; Score 154; DB 6; Length 352; Best Local Similarity 93.5%; Pred. No. 2.4e-14; Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Db 93.9% PRELIMINARY; PRT; 352 AA. RN Q95NC5 ID Q95NC5 AC Q95NC5; DT 01-DEC-2001 (TREMBLrel. 19, Created) - DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update) DR C-C chemokine receptor 5. GN CCR5. OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates. OX NCBI_TaxID=9590; RN SEQUENCE FROM N.A. RA Zhang Y., Ryder O.A., Zhang Y.; RT "Sequence comparison of the CCR5 gene in primates and primate phylogeny.", RT Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. DR EMBL; AF177884; RAK43367.1..1. DR GO; GO:0016021; C:integral to membrane; IEA. DR GO; GO:000472; F:receptor activity; IEA. DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA. DR InterPro; IPR000016; GPCR_Rhodpsn. DR Pfam; PF00001; 7tm_1..1. DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1_1..1. DR PROSITE; PS50262; G_PROTEIN_RECPEP_F1_2..1. KW Receptor. SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64; SQ Query Match 93.9%; Score 154; DB 6; Length 352; Best Local Similarity 93.5%; Pred. No. 2.4e-14; Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Db 93.9% PRELIMINARY; PRT; 352 AA. RN Q9TV49 ID Q9TV49 AC Q9TV49; DT 01-MAY-2000 (TREMBLrel. 13, Created) - DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update) DR CC chemokine receptor type 5 (C-C chemokine receptor 5). GN CCR5. OS Cercocebus galeritus (Agile mangabey). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; OC Cercopithecinae; Cercopithecus. NCBI_TaxID=9532; RN SEQUENCE FROM N.A. RP SPEAIN-4; RC MEDLINE=9335215; PubMed=10408730; RX RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C., RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.; RT "Mutations in CCR5-Coding sequences are not associated with SIV carrier status in African nonhuman primates.", AIDS Res. Hum. Retroviruses 15:931-939(1999)."; RL AIDS Res. Hum. Retroviruses 15:931-939(1999)."; RN [2]

SEQUENCE FROM N.A.
STRIDINE=04; PubMed=9335215; PubMed=10408730;
RX Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.C.,
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
carrier status in African nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=04;
RA Mueller-Trutwin M.C., Corbet S., Hansen J., Diop O.,
RA Georges-Courbot M.-C., Barré-Sinoussi F., Fomsgaard A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF0152220; ADP4013.1; -.
DR GO; GO:0016221; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF000001; ttm1; 1.
DR PRINTS; PR00237; GCBRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Receptor.
KW Receptor.
SQ SEQUENCE 352 AA; 40747 MW; 3A56B90D3528D94C CRC64;

Query Match 93.9%; Score 154; DB 6; Length 352;
Best Local Similarity 93.5%; Pred. No. 2.4e-14;
Matches 29; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MDYQVSSPTYDYYTSEPCOKINVQIAR 31
Db 1 MDYQVSSPTYDYYTSEPCOKINVQIAR 31

RESULT 15
097975 PRELIMINARY; PRT; 352 AA.
ID 097975
AC AC 097975
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor type 5.
GN CCR5.
OS Macaca arctoides (Stump-tailed macaque), and
OS Macaca assamensis (Assam's macaque) (Assam's monkey),
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca;
OX NCBI_TaxID:9540; 9551;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF075449; BAD19861.1; -.
DR GO; GO:0016221; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PRINTS; PR00237; GCBRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Receptor.
SQ SEQUENCE 352 AA; 40521 MW; 5P276C85909FACB2 CRC64;

Query Match 93.9%; Score 154; DB 6; Length 352;
Best Local Similarity 93.5%; Pred. No. 2.4e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Result No.	Score	Query	Match	Length	DB ID	Description
%						
1	164	100.0	87	3	US-09-087-232A-18	Sequence 18, Appl
2	164	100.0	100	3	US-09-087-232A-15	Sequence 15, Appl
3	164	100.0	184	4	US-09-083-752-4	Sequence 4, Appl
4	164	100.0	215	3	US-09-087-232A-17	Sequence 17, Appl
5	164	100.0	215	4	US-09-083-752-6	Sequence 6, Appl
6	164	100.0	352	3	US-09-087-232A-13	Sequence 13, Appl
7	164	100.0	352	3	US-09-086-105-14	Sequence 14, Appl
8	164	100.0	352	3	US-09-087-967A-2	Sequence 2, Appl
9	164	100.0	352	4	US-09-083-752-5	Sequence 5, Appl
10	164	100.0	352	4	US-09-086-105-14	Sequence 2, Appl
11	164	100.0	352	4	US-09-087-232A-13	Sequence 1, Appl
12	159	97.0	352	3	US-09-085-583-52	Sequence 52, Appl
13	158	96.3	352	4	US-09-085-185-52	Sequence 52, Appl
14	144	87.8	352	3	US-09-086-343D-2	Sequence 2, Appl
15	123	75.0	22	3	US-09-086-105-14	Sequence 4, Appl
16	113	68.9	20	2	US-09-089-291-32	Sequence 32, Appl
17	113	68.9	20	3	US-09-098-244-32	Sequence 32, Appl
18	113	68.9	20	4	US-09-086-105-14	Sequence 32, Appl
19	113	68.9	20	4	US-09-087-314-32	Sequence 32, Appl
20	113	68.9	20	4	US-09-087-395-32	Sequence 32, Appl
21	105	64.0	28	3	US-09-086-105-16	Sequence 6, Appl
22	64.0	354	4	US-09-074-98A-2	Sequence 2, Appl	
23	81.5	49.7	26	4	US-09-131-822A-14	Sequence 14, Appl
24	52	31.7	158	4	US-09-621-974-13	Sequence 7413, Appl
25	51	31.1	705	2	US-09-663-56A-19	Sequence 19, Appl
26	51	31.1	705	2	US-09-023-610-19	Sequence 19, Appl
27	51	705	2	US-09-288-065A-19	Sequence 19, Appl	

RESULT 2
US-09-87-232A-15
; Sequence 15, Application US/09087232A
; General Information:
; Applicant: Quillent et al.
; Title of Invention: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; Number of Sequences: C23
; Correspondence Address:
; Addressee: Baker & Botts, L.L.P. attn. Lisa Kole
; Street: 30 Rockefeller Plaza
; City: New York
; State: New York
; ZIP: 10112
; Computer Readable Form:
; Computer: IBM PC compatible
; Operating System: PC-DOS/MS-DOS
; Software: Patent In Release #1.0, Version #1.30 (EPO)
; Current Application Data:
; Application Number: US/09/087,232A
; Filing Date: 28 MAY 1998
; Classification: 435
; Prior Application Data:
; Filing Date: 30 MAY 1997
; Attorney/Agent Information:
; Name: KOLE, LISA B.
; Registration Number: 35,225
; Reference/Docket Number: AP 31115
; Telecommunication Information:
; Telephone: (212) 408-2828
; Telefax: (212) 765-2519
; Information for Seq ID No: 15:
; Sequence Characteristics:
; Length: 100 amino acids
; Type: amino acid
; Topology: linear
; Molecule Type: protein
; US-09-087-232A-15

Query Match 100.0%; Score 164; DB 3; Length 100;
Best Local Similarity 100.0%; Pfd. No. 1.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 164; DB 3; Length 100;
Best Local Similarity 100.0%; Pfd. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 164; DB 4; Length 184;
Best Local Similarity 100.0%; Pfd. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIIDINYTSEPCOKINVQIAAR 31
Db 1 MDYQVSSPIIDINYTSEPCQKINVQIAAR 31

RESULT 4
US-09-087-232A-17
; Sequence 17, Application US/09087232A
; General Information:
; Patent No. 6152424-
; Computer: IBM PC compatible
; Operating System: PC-DOS/MS-DOS
; Software: Patent In Release #1.0, Version #1.30 (EPO)
; Current Application Data:
; Correspondence Address:
; Addressee: Baker & Botts, L.L.P. attn. Lisa Kole
; Street: 30 Rockefeller Plaza
; City: New York
; State: New York
; Country: USA
; Filing Date: 28 MAY 1998
; Classification: 435
; Computer Readable Form:
; Medium Type: Floppy disk
; Computer: IBM PC compatible
; Operating System: PC-DOS/MS-DOS
; Software: Patent In Release #1.0, Version #1.30 (EPO)
; Current Application Data:
; Filing Date: 28 MAY 1998
; Classification: 435
; Prior Application Data:
; Application Number: 60/048,057
; Filing Date: 30 MAY 1997
; Attorney/Agent Information:
; Name: KOLE, LISA B.
; Registration Number: 35,225
; Reference/Docket Number: AP 31115
; Telecommunication Information:
; Telephone: (212) 408-2828
; Telefax: (212) 765-2519
; Information for Seq ID No: 15:
; Sequence Characteristics:
; Length: 100 amino acids
; Type: amino acid
; Topology: linear
; Molecule Type: protein
; US-09-087-232A-15

Query Match 100.0%; Score 164; DB 3; Length 100;
Best Local Similarity 100.0%; Pfd. No. 1.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 164; DB 3; Length 100;
Best Local Similarity 100.0%; Pfd. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 164; DB 4; Length 184;
Best Local Similarity 100.0%; Pfd. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDYQVSSPIIDINYTSEPCOKINVQIAAR 31
Db 1 MDYQVSSPIIDINYTSEPCQKINVQIAAR 31

RESULT 3
US-08-833-752-4
; Sequence 4, Application US/080833752
; General Information:
; Applicant: SAMSON, MICHEL
; Applicant: PARMENTIER, MARC
; Applicant: VASSART, GILBERT
; Applicant: LIBERT, FREDERICK
; Title of Invention: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; Title of Invention: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; Number of Sequences: 17
; Correspondence Address:
; Addressee: Knobbe, Martens, Olson & Bear
; Street: 620 Newport Center Drive
; City: Newport Beach
; State: CA
; Country: U.S.A.
; ZIP: 92660

Query Match Best Local Similarity 100.0%; Score 164; DB 3; Length 215;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/087-232A
 FILING DATE: 28 MAY 1998
 CLASSIFICATION: 435
 PRIORITY INFORMATION:
 Application No. 6448375
 Title of Invention: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
 Number of Sequences: 17
 Correspondence Address:
 Addressee: Knobbe, Martens, Olson & Bear
 Street: 620 Newport Center Drive 16th Floor
 City: Newport Beach
 State: CA
 Country: U.S.A.
 Zip: 92660
 Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM PC compatible
 Operating System: PC-DOS/MS-DOS
 Software: PatentIn Release #1.0, Version #1.25 (BPO)
 Current Application Data:
 Application Number: US/08/833,752
 Filing Date: 9-APR-1997
 Attorney/Agent Information:
 Name: Altman, Daniel E
 Registration Number: 34,115
 Reference/DoCKET NUMBER: 34,115
 Information for SEQ ID NO: 6:
 Sequence Characteristics:
 Length: 215 amino acids
 Type: amino acid
 Topology: linear
 Molecule Type: protein
 US-08-833-752-6

Query Match Best Local Similarity 100.0%; Score 164; DB 4; Length 215;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/861,105
 FILING DATE:
 Classification: 436
 Prior Application Data:
 Application Number: US 08/666,020
 Filing Date: 19-JUN-1996
 Classification: 436
 Prior Application Data:

RESULT 5
 US-08-833-752-6
 Sequence 6, Application US/08833752
 General Information:
 Applicant: SAMSON, MICHEL
 Applicant: VASSART, GILBERT
 Applicant: LIBERT, FREDERICK
 Title of Invention: ACTIVE AND INACTIVE CC-MOLECULES ENCODING SAID RECEPTOR
 Number of Sequences: 17
 Correspondence Address:
 Addressee: Knobbe, Martens, Olson & Bear
 Street: 620 Newport Center Drive 16th Floor
 City: Newport Beach
 State: CA
 Country: U.S.A.
 Zip: 92660
 Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM PC compatible
 Operating System: PC-DOS/MS-DOS
 Software: PatentIn Release #1.0, Version #1.25 (BPO)
 Current Application Data:
 Application Number: US/08/833,752
 Filing Date: 9-APR-1997
 Attorney/Agent Information:
 Name: Altman, Daniel E
 Registration Number: 34,115
 Reference/DoCKET NUMBER: 34,115
 Information for SEQ ID NO: 6:
 Sequence Characteristics:
 Length: 215 amino acids
 Type: amino acid
 Topology: linear
 Molecule Type: protein
 US-08-833-752-6

Query Match Best Local Similarity 100.0%; Score 164; DB 4; Length 215;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/861,105
 FILING DATE:
 Classification: 436
 Prior Application Data:
 Application Number: US 08/666,020
 Filing Date: 19-JUN-1996
 Classification: 436
 Prior Application Data:

RESULT 6
 US-09-087-232A-13
 Sequence 13, Application US/09087232A
 Patent No. 6153431
 General Information:
 Applicant: Quillent et al.
 Title of Invention: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
 Title of Invention: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
 Number of Sequences: 23
 Correspondence Address:
 Addressee: Baker & Botts, L.L.P. attn. Lisa Kole
 Street: 30 Rockefeller Plaza
 City: New York
 State: New York
 Country: USA

APPLICATION NUMBER: US 08/227,319
 FILING DATE: 13-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Eng., David A.
 REGISTRATION NUMBER: 26,742
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-87-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US 08-861-105-14

Query Match Similarity 100.0%; Score 164; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MDYQVSSPIYDINYTTSEPCOKINVQIAAR 31
 Db 1 MDYQVSSPIYDINYTTSEPCQINVQIAAR 31

RESULT 8
 US-08-575-967A-2
 Sequence 2, Application US/08575967A
 Patent No. 6,265,844
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Gray et al.
 TITLE OF INVENTION: Chemokine Receptor Materials and Methods
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Marshall, O'Toole, Gerstein, Murray & Borun.
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/575, 967A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: 6,265,844 and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 32918
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-485-1900
 TELEFAX: 206-485-1662
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: / = "BBC amino acid sequence"
 US-08-575-967A-2
 Query Match

Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MDYQVSSPIYDINYTTSEPCOKINVQIAAR 31
 Db 1 MDYQVSSPIYDINYTTSEPCQINVQIAAR 31
 RESULT 9
 US-08-833-752-5
 Sequence 5, Application US/08833752
 Patent No. 6448375
 GENERAL INFORMATION:
 APPLICANT: SAMSON, MICHEL
 PARMENTIER, MARC
 APPLICANT: VASSART, GILBERT
 APPLICANT: LIBERT, FREDERICK
 TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/833,752
 FILING DATE: 9-APR-1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Altman, Daniel E.
 REGISTRATION NUMBER: 34,115
 REFERENCE DOCKET NUMBER:
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-833-752-5
 Query Match Similarity 100.0%; Score 164; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 5.4e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MDYQVSSPIYDINYTTSEPCOKINVQIAAR 31
 Db 1 MDYQVSSPIYDINYTTSEPCQINVQIAAR 31
 RESULT 10
 US-09-502-783A-2
 Sequence 2, Application US/09502783A
 Patent No. 6511826
 GENERAL INFORMATION:
 APPLICANT: Li, Yi
 APPLICANT: Rubin, Steven M.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRE)
 FILE REFERENCE: 1488.115006
 CURRENT APPLICATION NUMBER: US/09/502,783A
 CURRENT FILING DATE: 2001-08-23
 PRIORITY APPLICATION NUMBER: 08/466,343
 PRIORITY FILING DATE: 1995-06-06
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn version 3.0

Query Match ; REFERENCE/DOCKET NUMBER: MNI-044
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2 ; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-52

Query Match ; REFERENCE/DOCKET NUMBER: MNI-044
; LENGTH: 352;
; Best Local Similarity 96.8%; Score 159; DB 3; Length 352;
; Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 11 ;
US-09-796-202-1 ; Sequence 1, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; ATTORNEY: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match ; REFERENCE/DOCKET NUMBER: MNI-044
; LENGTH: 352;
; Best Local Similarity 100.0%; Score 164; DB 4; Length 352;
; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy : 1 MDYQVSSPIYDINYTTSEPCQKINVKQIAAR 31
Db : 1 MDYQVSSPIYDINYTTSEPCQKINVKQIAAR 31

RESULT 13 ;
US-09-534-185-52 ; Sequence 52, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767 Molecules of the G Protein-Coupled
; Reptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match ; REFERENCE/DOCKET NUMBER: MNI-044
; LENGTH: 352;
; Best Local Similarity 96.8%; Score 159; DB 4; Length 352;
; Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy : 1 MDYQVSSPIYDINYTTSEPCQKINVKQIAAR 31

Db 4 1 |||||||:|||||:|||||:|||||:|||||:|||||
 RESULT 14 1 MDYQSSPIYDIDYTSEPCOKINVQIAAR 31
 i Sequence 2, Application US/08466343D
 ; Patent No. 6025154
 GENERAL INFORMATION:
 APPLICANT: LI, YI
 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
 TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGMR10 (AS AMENDED)
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STEERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/A/466,343D
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-466-343D-2

US-09-517-605-5
 Query Match 87.8%; Pred. No. 6e-14;
 Best Local Similarity 90.3%;保守性 1; Mismatches 2; Indels 0; Gaps 0;
 Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 i Sequence 5, Application US/09517605
 ; Patent No. 6392567
 GENERAL INFORMATION:
 APPLICANT: Littman, Dan R.
 APPLICANT: Kwon, Douglas S.
 APPLICANT: van Kooyk, Yvette
 APPLICANT: Geijtenbeek, Theo
 TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
 CELLS
 FILE REFERENCE: 1049-1-017
 CURRENT APPLICATION NUMBER: US/09/517,605
 CURRENT FILING DATE: 2000-03-02
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5
 LENGTH: 352
 TYPE: PRT
 ORGANISM: Homo sapiens

Search completed: July 29, 2004, 13:30:40
 Job time : 19 secs
 US-09-517-605-5
 Query Match 87.8%; Pred. No. 6e-14;
 Best Local Similarity 90.3%;保守性 1; Mismatches 2; Indels 0; Gaps 0;
 Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 i Sequence 5, Application US/09517605
 ; Patent No. 6392567
 GENERAL INFORMATION:
 APPLICANT: Littman, Dan R.
 APPLICANT: Kwon, Douglas S.
 APPLICANT: van Kooyk, Yvette
 APPLICANT: Geijtenbeek, Theo
 TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
 CELLS
 FILE REFERENCE: 1049-1-017
 CURRENT APPLICATION NUMBER: US/09/517,605
 CURRENT FILING DATE: 2000-03-02
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5
 LENGTH: 352
 TYPE: PRT
 ORGANISM: Homo sapiens

RESULT 15
 US-09-517-605-5
 Query Match 96.3%; Pred. No. 4.5e-16; Length 352;
 Best Local Similarity 96.8%;保守性 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 i Sequence 5, Application US/09517605
 ; Patent No. 6392567
 GENERAL INFORMATION:
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